

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2005, 15:38:10 ; Search time 167 Seconds
(without alignments)
42.929 Million cell updates/sec

Title: US-10-663-215-5

Perfect score: 74

Sequence: 1 YETFSKLIKIFQDH 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	911	1	B3AT_HUMAN
2	68	91.9	849	2	Q912E7
3	68	91.9	927	1	B3AT_RAT
4	68	91.9	929	1	B3AT_MOUSE
5	64	86.5	466	2	Q991T5
6	64	86.5	1234	1	B3A2_RAT
7	64	86.5	1237	1	B3A2_MOUSE
8	64	86.5	1237	1	B3A2_RABIT
9	64	86.5	1237	2	Q7TFS4
10	63	85.1	622	2	Q9TU75
11	63	85.1	1087	2	Q6PJY3
12	63	85.1	1159	2	Q8TAG3
13	63	85.1	1217	2	Q7TIP5
14	63	85.1	1227	2	Q9UEY4
15	63	85.1	1232	2	Q9UEY5
16	63	85.1	1237	2	Q6SJP2
17	63	85.1	1238	1	B3A2_CAVPO
18	63	85.1	1241	1	B3A2_HUMAN
19	63	85.1	1241	2	Q99654
20	63	85.1	1241	2	Q9UEY6
21	62	83.8	812	2	Q8JFT9
22	62	83.8	904	2	Q7ZZV6
23	62	83.8	905	2	Q7ZZJ7
24	62	83.8	1219	2	Q90710
25	61	82.4	81	2	Q9TRC8
26	61	82.4	663	2	Q9TUQ1
27	61	82.4	855	2	Q9TUQ0
28	61	82.4	930	2	Q9XSW5
29	55	74.3	147	2	Q9GKN5
30	55	74.3	898	2	Q7TIP6
31	54	73.0	908	2	Q6JRS1

32	54	73.0	912	2	Q91452	Q91452 oncorhynchu
33	54	73.0	918	1	B3AT_ONCMY	P32847 oncorhynchu
34	53	71.6	922	1	B3AT_CHICK	P15575 gallus gall
35	53	71.6	1030	2	Q9ERP4	Q9ERP4 mus musculus
36	53	71.6	1227	1	B3A3_MOUSE	P16283 mus musculus
37	53	71.6	1227	1	B3A3_RAT	P23348 rattus norv
38	53	71.6	1227	2	Q9ERP5	Q9ERP5 mus musculus
39	53	71.6	1233	1	B3A3_RABIT	O18917 oryctolagus
40	53	71.6	1239	2	Q68EG4	Q68EG4 mus musculus
41	52	70.3	357	2	Q13717	Q13717 homo sapien
42	52	70.3	357	2	Q99416	Q99416 homo sapien
43	52	70.3	1232	1	B3A3_HUMAN	P48751 homo sapien
44	50	67.6	844	2	Q90579	Q90579 gallus gall
45	47	63.5	1055	2	Q8H6B1	Q8H6B1 zea mays (m

ALIGNMENTS

RESULT 1
B3AT_HUMAN
ID B3AT_HUMAN STANDARD; PRT; 911 AA.
AC P02730;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
GN (CD233 antigen).
GN Name=SLC4A1; Synonyms=AE1, DI, EPB3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9083213; PubMed=2594752;
RA Lux S.E., John K.M., Kopito R.R., Lodish H.F.;
RT "Cloning and characterization of band 3, the human erythrocyte anion-
exchange protein (AE1).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:9089-9093(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=89134172; PubMed=3223947;
RA Tanner M.J.A., Martin P.G., High S.;
RT "The complete amino acid sequence of the human erythrocyte membrane
anion-transport protein deduced from the cDNA sequence.";
RL Biochem. J. 256:703-712(1988).
RN [3]
RP SEQUENCE OF 1-199; 220-292 AND 347-370.
RX MEDLINE=90001294; PubMed=2790053; DOI=10.1016/0167-4838(89)90116-7;
RA Yannoukakos D., Vasseur C., Blouquit Y., Bureau E., Wajzman H.;
RT "Primary structure of the cytoplasmic domain of human erythrocyte
protein band 3. Comparison with its sequence in the mouse.";
RL Biochim. Biophys. Acta 998:43-49(1989).
RN [4]
RP SEQUENCE OF 1-201.
RX MEDLINE=83238395; PubMed=6345535;
RA Kaul R.K., Murthy S.N.P., Reddy A.G., Steck T.L., Kohler H.;
RT "Amino acid sequence of the N alpha-terminal 201 residues of human
erythrocyte membrane band 3.";
RL J. Biol. Chem. 258:7981-7990(1983).
RN [5]
RP SEQUENCE OF 1-3.
RX MEDLINE=79027186; PubMed=701248;
RA Drickamer L.K.;
RT "Orientation of the band 3 polypeptide from human erythrocyte
membranes. Identification of NH2-terminal sequence and site of
carbohydrate attachment.";
RL J. Biol. Chem. 253:7242-7248(1978).
RN [6]
RP SEQUENCE OF 559-630.
RX MEDLINE=83308584; PubMed=6615451;

RA Brock C.J., Tanner M.J.A., Kempf C.;
RT "The human erythrocyte anion-transport protein. Partial amino acid
RT sequence, conformation and a possible molecular mechanism for anion
RT exchange."; Biochem. J. 213:577-586 (1983).
RL [7]
RN SEQUENCE OF 834-911.
RP MEDLINE=88228050; PubMed=3372523;
RA Kawano Y., Okubo K., Tokunaga F., Miyata T., Iwanaga S., Hamasaki N.;
RT "Localization of the pyridoxal phosphate binding site at the COOH-
RT terminal region of erythrocyte band 3 protein."; J. Biol. Chem. 263:8232-8238 (1988).
RL [8]
RN ROLE OF GLU-681, AND SEQUENCE OF 665-688.
RP MEDLINE=92332495; PubMed=1352774;
RA Jennings M.L., Smith J.S.;
RT "Anion-proton cotransport through the human red blood cell band 3
RT protein. Role of glutamate 681."; J. Biol. Chem. 267:13964-13971 (1992).
RL [9]
RN PALMITOYLATION OF CVS-843
RP MEDLINE=91358422; PubMed=1885574;
RA Okubo K., Hamasaki N., Hara K., Kageura M.;
RT "Palmitoylation of cysteine 69 from the COOH-terminal of band 3
RT protein in the human erythrocyte membrane. Acylation occurs in the
RT middle of the consensus sequence of P-I-IIICLAVL found in band 3
RT protein and G2 protein of Rift Valley fever virus."; J. Biol. Chem. 266:16420-16424 (1991).
RL [10]
RN PHOSPHORYLATION SITES TYR-8; TYR-21; TYR-359 AND TYR-904.
RP MEDLINE=20400020; PubMed=10942405;
RA Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono E.,
RA Pinna L.A., Donella-Deana A.;
RT "Sequential phosphorylation of protein band 3 by Syk and Lyn tyrosine
RT kinases in intact human erythrocytes: identification of primary and
RT secondary phosphorylation sites."; Blood 96:1550-1557 (2000).
RL [11]
RN VARIANT MEMPHIS GLU-56
RP MEDLINE=91329825; PubMed=1678289;
RA Yannoukakos D., Vassess C., Driancourt C., Blouquit Y., Delauney J.,
RA Wajcman H., Bureau E.;
RT "Human erythrocyte band 3 polymorphism (band 3 Memphis):
RT characterization of the structural modification (Lys 56-->Glu) by
RT protein chemistry methods."; Blood 78:1117-1120 (1991).
RL [12]
RN VARIANT HE 400-ALA--ALA-408 DEL, AND VARIANT MEMPHIS GLU-56.
RP MEDLINE=92107882; PubMed=1722314;
RA Jarolim P., Palek J., Anato D., Hassan K., Sapak P., Nurse G.T.,
RA Rubin H.L., Zhai S., Sahr K.E., Liu S.-C.;
RT "Deletion in erythrocyte band 3 gene in malaria-resistant Southeast
RT Asian ovalocytosis."; Proc. Natl. Acad. Sci. U.S.A. 88:11022-11026 (1991).
RL [13]
RN VARIANT HS ARG-327.
RP MEDLINE=92329950; PubMed=1378323;
RA Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C.,
RA Cohen C.M.;
RT "Band 3 Tuscaloosa: Pro-327-->Arg substitution in the cytoplasmic
RT domain of erythrocyte band 3 protein associated with spherocytic
RT hemolytic anemia and partial deficiency of protein 4.2."; Blood 80:523-529 (1992).
RL [14]
RN VARIANT HE 400-ALA--ALA-408 DEL.
RP MEDLINE=92167271; PubMed=1538405;
RA Schofield A.B., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M.,
RA Nash G.B., Dluzewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M.,
RA Gratzner W.B.;
RT "Basis of unique red cell membrane properties in hereditary
RT ovalocytosis."; J. Mol. Biol. 223:949-958 (1992).
RL [15]

RP VARIANT HS LEU-868.
RX MEDLINE=93343855; PubMed=8343110;
RA Bruce L.J., Kay M.M., Lawrence C., Tanner M.J.;
RT "Band 3 HI, a human red-cell variant associated with acanthocytosis
RT and increased anion transport, carries the mutation Pro-868-->Leu in
RT the membrane domain of band 3."; Biochem. J. 293:317-320 (1993).
RL [16]
RN VARIANT MONTEFIORE LYS-40.
RP MEDLINE=93229758; PubMed=8471774;
RA Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L.,
RA Schwartz R.S.;
RT "Human erythrocyte protein 4.2 deficiency associated with hemolytic
RT anemia and a homozygous 40 glutamic acid-->lysine substitution in the
RT cytoplasmic domain of band 3 (band 3Montefiore)."; Blood 81:2155-2165 (1993).
RL [17]
RN VARIANT BLOOD GROUP DI(A)/MEMPHIS-II.
RP MEDLINE=94266802; PubMed=8206915;
RA Bruce L.J., Anstee D.J., Spring F.A., Tanner M.J.;
RT "Band 3 Memphis variant II: Altered stilbene disulfonate binding and
RT the Diego (Dia) blood group antigen are associated with the human
RT erythrocyte band 3 mutation Pro-854-->Leu."; J. Biol. Chem. 269:16155-16158 (1994).
RL [18]
RN VARIANT BLOOD GROUP WR(A).
RP MEDLINE=95111140; PubMed=7812009;
RA Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson S.,
RA Tanner M.J.;
RT "Changes in the blood group Wright antigens are associated with a
RT mutation at amino acid 658 in human erythrocyte band 3: a site of
RT interaction between band 3 and glycophorin A under certain
RT conditions."; Blood 85:541-547 (1995).
RL [19]
RN VARIANTS HS GLN-760; TRP-760; CVS-808 AND TRP-870.
RP MEDLINE=95134893; PubMed=7530501;
RA Jarolim P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S.,
RA Alper S.L., Brugnara C., Wichterle H., Palek J.;
RT "Mutations of conserved arginines in the membrane domain of erythroid
RT band 3 lead to a decrease in membrane-associated band 3 and to the
RT phenotype of hereditary spherocytosis."; Blood 85:634-640 (1995).
RL [20]
RN VARIANT HS ASP-771.
RP MEDLINE=96136073; PubMed=8547122;
RA Maillet P., Vallier A., Reinhardt W.H., Wyss E.J., Ott P., Texier P.,
RA Baklouti F., Tanner M.J., Delaunay J., Alloisio N.;
RT "Band 3 Chur: a variant associated with band 3-deficient hereditary
RT spherocytosis and substitution in a highly conserved position of
RT transmembrane segment 11."; Br. J. Haematol. 91:804-810 (1995).
RL [21]
RN VARIANTS HS ASP-285; GLU-455; PRO-707; PRO-834 AND MET-837.
RP MEDLINE=97099297; PubMed=8943874;
RA Jarolim P., Murray J.L., Rubin H.L., Taylor W.M., Prchal J.T.,
RA Ballas S.K., Snyder L.M., Chrobak L., Melrose W.D., Brabec V.,
RA Palek J.;
RT "Characterization of 13 novel band 3 gene defects in hereditary
RT spherocytosis with band 3 deficiency."; Blood 88:4366-4374 (1996).
RL [22]
RN VARIANTS HS LYS-40; CVS-518 AND MET-663 DEL.
RP MEDLINE=96225450; PubMed=8640229;
RA Eder S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
RA Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,
RA Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
RT "Ankyrin-1 mutations are a major cause of dominant and recessive
RT hereditary spherocytosis."; Nat. Genet. 13:214-218 (1996).
RL [23]
RN VARIANTS HS SER-147 AND MET-488.
RP MEDLINE=97351102; PubMed=9207478;

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OM protein - protein search, using sw model

Run on: August 26, 2005, 15:33:50 ; Search time 164 Seconds
(without alignments)
33.016 Million cell updates/sec

Title: US-10-663-215-5

Perfect score: 74

Sequence: 1 YETFSKLKIFQDH 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1990s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	58	2 AAW01093	Aaw01093 Exofacial
2	74	100.0	58	4 AAB74884	Aab74884 Human ban
3	74	100.0	80	4 AAU30823	Aau30823 Novel hum
4	74	100.0	911	2 AAR15355	Aar15355 Human ery'
5	74	100.0	911	2 AAW90263	Aaw90263 A. tigrin
6	74	100.0	911	4 AAB46914	Aab46914 Human ery
7	74	100.0	911	5 AAE29343	Aae29343 Human Ban
8	74	100.0	911	5 AAE29344	Aae29344 Human Ban
9	74	100.0	911	7 ADE56706	Ades6706 Human Pro
10	74	100.0	911	7 ADJ68197	Adj68197 Human hea
11	74	100.0	911	7 ADJ86694	Adj86694 Human hea
12	74	100.0	911	8 ADL06510	Adl06510 Human tum
13	74	100.0	933	8 ABM84084	Abm84084 Human dia
14	74	100.0	962	4 AAU30825	Aau30825 Novel hum
15	68	91.9	927	7 ADE56704	Ades6704 Rat Prote
16	65	87.8	50	5 ABB84592	Abb84592 Human cat
17	64	86.5	1234	7 ADE56763	Ades6763 Rat Prote
18	64	86.5	1234	7 ADE56753	Ades6753 Rat Prote
19	64	86.5	1234	7 ADE56759	Ades6759 Rat Prote
20	64	86.5	1234	7 ADE56757	Ades6757 Rat Prote
21	64	86.5	1237	8 ADF72495	Adf72495 Osteoclas
22	63	85.1	1227	8 ADF72499	Adf72499 Osteoclas
23	63	85.1	1232	8 ADF72501	Adf72501 Osteoclas
24	63	85.1	1240	2 AAW90262	Aaw90262 A. tigrin
25	63	85.1	1241	7 ADE56755	Ades6755 Human Pro

26	63	85.1	1241	7 ADE56761	Ades6761 Human Pro
27	63	85.1	1241	7 ADE57913	Ades7913 Human Pro
28	63	85.1	1241	8 ADF72497	Adf72497 Osteoclas
29	61	82.4	713	7 ADL25374	Adl25374 HCO3-tran
30	53	71.6	1030	2 AAW90261	Aaw90261 A. tigrin
31	52	70.3	812	8 ADH22554	Adh22554 Human tra
32	52	70.3	1153	8 ABM83555	Abm83555 Human dia
33	52	70.3	1198	8 ABM83554	Abm83554 Human dia
34	52	70.3	1207	8 ABM83553	Abm83553 Human dia
35	52	70.3	1225	8 ABM83552	Abm83552 Human dia
36	52	70.3	1232	7 ADE80764	Ades0764 Microsate
37	52	70.3	1234	8 ABM83551	Abm83551 Human dia
38	52	70.3	1259	7 ADJ70768	Adj70768 Human hea
39	51	68.9	17	2 AAW18597	Aaw18597 Aged band
40	47	63.5	15	4 AAB74851	Aab74851 Band 3 pr
41	44	59.5	779	8 ADJ48804	Adj48804 Oil-assoc
42	44	59.5	1060	8 ADJ48805	Adj48805 Oil-assoc
43	42	56.8	316	8 ADJ48467	Adj48467 Maize Oil
44	42	56.8	318	8 ADJ50288	Adj50288 Oil-assoc
45	42	56.8	318	8 ADJ48728	Adj48728 Oil-assoc

ALIGNMENTS

RESULT 1

AAW01093

ID AAW01093 standard; peptide; 58 AA.

AC AAW01093;

DT 08-MAY-1997 (first entry)

DE Exofacial region loop 3 of band 3 protein (residues 520-577).

KW Anion transporter band 3 protein; endothelial adhesion; red blood cell;
KW cytoplasmic domain; erythrocyte; exofacial loop; epitope; antibody;
KW mammal; Plasmodium falciparum infection; sickle cell disease; diabetes;
KW band 3; thalasassaemia; anaemia; therapy.

OS Synthetic.

XX WO9629086-A1.

XX 26-SEP-1996.

PF 07-MAR-1996; 96WO-US003180.

XX 17-MAR-1995; 95US-00405647.

PA (REGC) UNIV CALIFORNIA.

PI Sherman IW, Crandall IE, Shohet SB, Thevenin BJ;

XX WPI; 1996-442944/44.

PT Peptide(s) with amino acid motifs in band 3 - used for reducing the
PT adhesiveness of red blood cells for treating malaria, sickle cell
PT disease, thalasassaemia or diabetes.

XX Example 2; Page 20; 48pp; English.

CC AAW01053-W01095 represent peptides isolated from (or based on) regions of
CC the anion transporter band 3 protein. The band 3 protein is present in a
CC million copies per red blood cell, in the form of monomers, dimers, or
CC tetramers. Band 3 protein has two distinct domains, a 43 kD water-soluble
CC cytoplasmic domain, and a 55 kD membrane spanning domain. In an number of
CC otherwise-unrelated conditions (such as malaria, and diabetes), there are
CC modifications in band 3, such that there is clustering and a change in
CC the conformation of the protein. Due to this change in protein
CC conformation (and by the exposure of cryptic adhesive sites), the
CC normally non-adherent erythrocyte becomes a cell with enhanced
CC endothelial adhesiveness. These sequences were found in the putative

CC exofacial loops of band 3, and are epitopes for antibody binding. These
CC sequences compete with the altered band 3 protein, and thereby block the
CC adhesiveness of the red blood cells. The peptides can be used for
CC reducing the adhesiveness of red blood cells in a mammalian patient
CC characterised by a condition selected from Plasmodium falciparum
CC infection, sickle cell disease, thalassaemia and diabetes
XX
XX SQ Sequence 58 AA;

Query Match 100.0%; Score 74; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 5.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YETFSKLKIFQDH 14
|||||
DB 15 YETFSKLKIFQDH 28

RESULT 2
AAB74884
ID AAB74884 standard; peptide; 58 AA.

XX AC AAB74884;

XX DT 19-JUN-2001 (first entry)

XX DE Human band 3 protein predicted exofacial region loop 3 SEQ ID NO:41.

XX KW Anti-Plasmodium falciparum; interaction inhibitor; band 3 protein;
XX thrombolysis; thrombolytic; fibrinolytic; acute myocardial infarction;
XX lysis; ventricular function; congestive heart failure; mortality;
XX acute arterial thrombosis; embolism; thrombosis; cerebral sinus.

XX OS Homo sapiens.

XX XX US6191103-B1.

XX PD 20-FEB-2001.

XX PF 05-DEC-1997; 97US-00985499.

XX PR 05-DEC-1997; 97US-00985499.

XX PA (REGC) UNIV CALIFORNIA.
XX PA (BLOO-) CENT BLOOD RES.

XX PI Shohet SB, Sherman I, Von Andrian U;

XX XX WPI; 2001-307101/32.

XX PT Enhancing thrombolysis in mammals comprises administering an inhibitor of
XX protein band 3-ligand interaction.

XX PS Disclosure; Col 7; 23pp; English.

XX CC The present invention describes a method for enhancing thrombolysis in a
XX mammal. The method comprises the administration to the mammal an amount
XX of an inhibitor (I) of protein band 3-ligand interaction sufficient to
XX enhance thrombolysis. (I) has thrombolytic activity. The method is useful
XX for enhancing thrombolysis in a mammal. (I) is useful for enhancing
XX fibrinolytic or thrombolytic activity, in the management of acute
XX myocardial infarction, for lysis of intracoronary thrombi, for
XX improvement of ventricular function, for reduction of congestive heart
XX failure, for reduction of mortality, for the lysis of pulmonary emboli
XX blocking blood flow to one or more lobes of the lung, for the lysis of
XX acute arterial thrombosis and embolism, for the lysis of thrombosis in
XX deep veins or in cerebral sinuses, to reopen i.v. catheters obstructed by
XX clotted blood or fibrin, to prevent clot formation of lysing clots, to
XX prevent clotting in blood samples drawn from patients for clinical
XX testing and to prevent the recurrence of thrombosis in patients by
XX prophylactic administration. The present sequence represents a human band
XX 3 protein predicted exofacial region loop peptide, which is used in the
XX exemplification of the present invention

XX SQ Sequence 58 AA;

Query Match 100.0%; Score 74; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 5.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YETFSKLKIFQDH 14
|||||
DB 15 YETFSKLKIFQDH 28

RESULT 3
AAU30823
ID AAU30823 standard; protein; 80 AA.

XX AC AAU30823;

XX DT 18-DEC-2001 (first entry)

XX DE Novel human secreted protein #1314.

XX KW Human; vaccination; gene therapy; nutritional supplement;
XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX OS Homo sapiens.

XX XX WO200179449-A2.

XX PD 25-OCT-2001.

XX PF 16-APR-2001; 2001WO-US008656.

XX PR 18-APR-2000; 2000US-00552929.

XX PR 26-JAN-2001; 2001US-00770160.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-611725/70.

XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic
XX vaccination, testing and therapy.

XX PS Claim 20; Page 353; 765pp; English.

XX CC The invention relates to novel human secreted polypeptides. The
XX polypeptides and antibodies to the polypeptides are useful for
XX determining the presence of or predisposition to a disease associated
XX with altered levels of polypeptide. The polypeptides are also useful for
XX identifying agents (agonists and antagonists) that bind to them. Cells
XX expressing the proteins are useful for identifying a therapeutic agent
XX for use in treatment of a pathology related to aberrant expression or
XX physiological interactions of the polypeptide. Vectors comprising the
XX nucleic acids encoding the polypeptides and cells genetically engineered
XX to express them are also useful for producing the proteins. The proteins
XX are useful in genetic vaccination, testing and therapy, and can be used
XX as nutritional supplements. They may be used to increase stem cell
XX proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
XX and/or nerve tissue growth or regeneration; immune suppression and/or
XX stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
XX AAU29510-AAU33304 represent the amino acid sequences of novel human
XX secreted proteins of the invention

XX SQ Sequence 80 AA;

Query Match 100.0%; Score 74; DB 4; Length 80;
Best Local Similarity 100.0%; Pred. No. 7.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YETFSKLKIFQDH 14

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OM protein - protein search, using sw model

Run on: August 26, 2005, 15:39:16 ; Search time 39 Seconds
(without alignments)
34.539 Million cell updates/sec

Title: US-10-663-215-5

Perfect score: 74

Sequence: 1 YETFSKLIKIFQDH 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	911	1 B3HU	band 3 anion trans
2	68	91.9	848	2 A33810	band 3 anion trans
3	68	91.9	929	2 A25314	band 3 protein - m
4	64	86.5	1234	2 A34911	band 3-related pro
5	64	86.5	1237	2 A56764	band 3-related pro
6	64	86.5	1237	2 A31789	band 3-related pro
7	63	85.1	865	2 A25104	band 3 protein, no
8	63	85.1	1240	2 S21086	anion exchange pro
9	54	73.0	912	2 S59861	band 3 anion trans
10	54	73.0	918	2 S24318	band 3 anion trans
11	53	71.6	922	2 A30816	band 3 anion trans
12	53	71.6	1030	2 A42497	anion exchanger 3,
13	53	71.6	1227	2 A33638	erythrocyte anion
14	53	71.6	1227	2 B34911	band 3-related pro
15	52	70.3	357	2 S31828	band 3 anion trans
16	52	70.3	1232	2 S38496	anion exchanger 3
17	50	67.6	844	2 I50159	anion transporter
18	43	58.1	409	2 T19326	hypothetical prote
19	43	58.1	449	2 T08309	conserved hypothet
20	43	58.1	929	2 T28927	hypothetical prote
21	42	56.8	1044	2 T37568	hypothetical prote
22	41	55.4	383	2 T23057	hypothetical prote
23	41	55.4	550	2 C84582	hypothetical prote
24	40.5	54.7	241	2 C64612	2-hydroxy-6-oxohp
25	40.5	54.7	241	2 B71903	hypothetical prote
26	40	54.1	257	2 G84109	two-component resp
27	40	54.1	349	2 T24308	hypothetical prote
28	40	54.1	509	2 T30861	traj protein - Sal
29	40	54.1	1427	2 S74293	SRB8 protein - yea

RESULT 1

B3HU

band 3 anion transport protein, erythrocyte - human

N;Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion exchange

C;Species: Homo sapiens (man)

C;Date: 03-Aug-1984 #sequence revision 03-Oct-1995 #text change 09-Jul-2004

C;Accession: A36218; S03074; I39408; I39409; A92237; A26507; A92430; A90323; A28079; S05:

R;Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F.

Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9093, 1989

A;Title: Cloning and characterization of band 3, the human erythrocyte anion-exchange pr

A;Reference number: A36218; MUID:90083213; PMID:2594752

A;Accession: A36218

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-911 <LUX>

A;Cross-references: UNIPROT:P02730; GB:M27819; NID:G178215; PIDN:AAA35514.1; PID:G178216

R;Tanner, M.J.A.; Martin, P.G.; High, S.

Biochem. J. 256, 703-712, 1988

A;Title: The complete amino acid sequence of the human erythrocyte membrane anion-transp

A;Reference number: S03074; MUID:89134172; PMID:3223947

A;Accession: S03074

A;Molecule type: mRNA

A;Residues: 1-55, 'E', 57-911 <TAN>

A;Cross-references: EMBL:X12609; NID:G28713; PIDN:CAA31128.1; PID:G28714

R;Shove, L.C.; Ballantine, M.; Huebner, K.

Genomics 1, 71-76, 1987

A;Title: Localization of the gene for the erythroid anion exchange protein, band 3 (EMP

A;Reference number: I39408; MUID:88031311; PMID:3478298

A;Accession: I39408

A;Molecule type: DNA

A;Residues: 37-56 <SHOI>

A;Cross-references: GB:M16978; NID:G178217; PIDN:AAA51670.1; PID:G178220

A;Accession: I39409

A;Molecule type: DNA

A;Residues: 118-161 <SHO2>

A;Cross-references: GB:M16979; NID:G178218; PIDN:AAA51671.1; PID:G553169

R;Drickamer, L.K.

J. Biol. Chem. 253, 7242-7248, 1978

A;Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. Identifi

A;Reference number: A92237; MUID:79027186; PMID:701248

A;Accession: A92237

A;Molecule type: protein

A;Residues: 1-3 <DRI>

R;Nawby, W.J.; Findlay, J.B.C.

Biochem. J. 205, 465-475, 1982

A;Title: Characterization and partial sequence of di-iodosulphophenyl isothiocyanate-binc

A;Reference number: A26507; MUID:83074521; PMID:7150226

A;Accession: A26507

A;Molecule type: protein

A;Residues: 437-473,360-364, 'D', 366-369 <MAW>

R;Kaul, R.K.; Murthy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, H.

J. Biol. Chem. 258, 7981-7990, 1983

C;Title: Amino acid sequence of the N(alpha)-terminal 201 residues of human erythrocyte A;Reference number: A92430; MUID:83238395; PMID:6345535
A;Accession: A92430
A;Molecule type: protein
A;Residues: 1-10,'D',12-68,'E',69-200 <KAU>
R;Brook, C.J.; Tanner, M.J.A.; Kempf, C.
Biochem. J. 213, 577-586, 1983
A;Title: The human erythrocyte anion-transport protein.
A;Reference number: A90323; MUID:83308584; PMID:6615451
A;Accession: A90323
A;Molecule type: protein
A;Residues: 553-630 <BRO>
A;Note: Lys-590 was shown to bind phenyl isothiocyanate, an inhibitor of anion transport
J;Kawano, Y.; Okubo, K.; Tokunaga, F.; Miyata, T.; Iwanaga, S.; Hamasaki, N.
J. Biol. Chem. 263, 8232-8238, 1988
A;Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal region of the human erythrocyte anion-transport protein.
A;Reference number: A28079; MUID:88228050; PMID:3372523
A;Accession: A28079
A;Molecule type: protein
A;Residues: 834-842,'X',844-911 <KAW>
A;Note: Lys-851 was shown to bind the affinity label pyridoxal phosphate, a substrate for the human erythrocyte anion-transport protein.
R;Yamoukakos, D.; Vasseur, C.; Blouquit, Y.; Bursaux, E.; Wajcman, H.
Biochim. Biophys. Acta 998, 43-49, 1989
A;Title: Primary structure of the cytoplasmic domain of human erythrocyte protein band 3
A;Reference number: S05523; MUID:90001294; PMID:2790053
A;Accession: S05523
A;Molecule type: protein
A;Residues: 1-201,220-292;307-308,'R',310-312,'S',314-329,'K',331-333;347-370 <YAN1>
R;Cobb, C.E.; Beth, A.H.
Biochemistry 29, 8283-8290, 1990
A;Title: Identification of the eosinyl-5-maleimide reaction site on the human erythrocyte protein band 3
A;Reference number: A35835; MUID:91070049; PMID:1701324
A;Accession: A35835
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-55,'E',57-69 <YAN2>
A;Note: sequence extracted from NCBI backbone (NCBIP:49829)
R;Kang, D.; Okubo, K.; Hamasaki, N.; Kuroda, N.; Shiraki, H.
J. Biol. Chem. 267, 19211-19217, 1992
A;Title: A structural study of the membrane domain of band 3 by tryptic digestion. Confirmed by X-ray crystallography.
A;Reference number: A44116; MUID:92406862; PMID:1527044
A;Accession: A44116
A;Status: preliminary
A;Molecule type: protein
A;Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826 <KAN>
A;Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:113821, NCBIP:113823, NCBIP:113825, NCBIP:113827, NCBIP:113829, NCBIP:113831, NCBIP:113833, NCBIP:113835, NCBIP:113837, NCBIP:113839, NCBIP:113841, NCBIP:113843, NCBIP:113845, NCBIP:113847, NCBIP:113849, NCBIP:113851, NCBIP:113853, NCBIP:113855, NCBIP:113857, NCBIP:113859, NCBIP:113861, NCBIP:113863, NCBIP:113865, NCBIP:113867, NCBIP:113869, NCBIP:113871, NCBIP:113873, NCBIP:113875, NCBIP:113877, NCBIP:113879, NCBIP:113881, NCBIP:113883, NCBIP:113885, NCBIP:113887, NCBIP:113889, NCBIP:113891, NCBIP:113893, NCBIP:113895, NCBIP:113897, NCBIP:113901, NCBIP:113903, NCBIP:113905, NCBIP:113907, NCBIP:113909, NCBIP:113911, NCBIP:113913, NCBIP:113915, NCBIP:113917, NCBIP:113919, NCBIP:113921, NCBIP:113923, NCBIP:113925, NCBIP:113927, NCBIP:113929, NCBIP:113931, NCBIP:113933, NCBIP:113935, NCBIP:113937, NCBIP:113939, NCBIP:113941, NCBIP:113943, NCBIP:113945, NCBIP:113947, NCBIP:113949, NCBIP:113951, NCBIP:113953, NCBIP:113955, 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OM protein - protein search, using sw model

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Total number of hits satisfying chosen parameters: 513545

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	43	58.1	702	4	US-09-248-796A-15814
7	41	55.4	567	4	US-09-328-352-7620
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25	38	51.4	630	4	US-09-360-545-67
26	37	50.0	99	1	US-08-202-389-36
27	37	50.0	431	4	US-09-248-796A-17260

ALIGNMENTS

RESULT 1
US-08-405-647B-41
; Sequence 41, Application US/08405647B
; Patent No. 6124262
; GENERAL INFORMATION:
; APPLICANT: Sherman, Irwin W.
; APPLICANT: Crandall, Ian E.
; APPLICANT: Sholet, Stephen B.
; APPLICANT: Thevenin, Bernard Jean-Marie
; TITLE OF INVENTION: Compositions and Methods for Reducing
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,647B
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 02307E-0697000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-405-647B-41

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Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Patent No. 6191103
; GENERAL INFORMATION:
; APPLICANT: Shohet, Stephen B.
; APPLICANT: Sherman, Irwin
; APPLICANT: von Andrian, Ulrich
; TITLE OF INVENTION: Methods for Enhancing Thrombolysis in a
; TITLE OF INVENTION: Mammal
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,499
; FILING DATE: 05-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hyman, Laurence J.
; REGISTRATION NUMBER: 35,551
; REFERENCE/DOCKET NUMBER: 02307E-084500US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-985-499-41

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Best Local Similarity 100.0%; Pred. No. 6.4e-06;
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Db      15 YETFSKLKIFQDH 28

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; Sequence 41, Application PC/TUS9603180
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University
; APPLICANT: of California
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REDUCING
; TITLE OF INVENTION: ADHESIVENESS OF DEFECTIVE RED BLOOD CELLS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 North Figueroa Street, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
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RESULT 4
US-08-985-499-8
; Sequence 8, Application US/08985499
; Patent No. 6191103
; GENERAL INFORMATION:
; APPLICANT: Shohet, Stephen B.
; APPLICANT: Sherman, Irwin
; APPLICANT: von Andrian, Ulrich
; TITLE OF INVENTION: Methods for Enhancing Thrombolysis in a
; TITLE OF INVENTION: Mammal
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,499
; FILING DATE: 05-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hyman, Laurence J.
; REGISTRATION NUMBER: 35,551
; REFERENCE/DOCKET NUMBER: 02307E-084500US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-985-499-8

Query Match 100.0%; Score 74; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
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Qy      1 YETFSKLKIFQDH 14
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US-08-985-499-8
; Sequence 8, Application US/08985499
; Patent No. 6191103
; GENERAL INFORMATION:
; APPLICANT: Shohet, Stephen B.
; APPLICANT: Sherman, Irwin
; APPLICANT: von Andrian, Ulrich
; TITLE OF INVENTION: Methods for Enhancing Thrombolysis in a
; TITLE OF INVENTION: Mammal
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,499
; FILING DATE: 05-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hyman, Laurence J.
; REGISTRATION NUMBER: 35,551
; REFERENCE/DOCKET NUMBER: 02307E-084500US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-985-499-8
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GenCore version 5.1.6
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SUMMARIES

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6	74	100.0	911	16	US-10-408-765A-500
7	74	100.0	911	16	US-10-643-795A-90
8	74	100.0	911	17	US-10-663-215-1
9	74	100.0	911	17	US-10-948-518-90
10	61	82.4	713	14	US-10-128-202-4
11	52	70.3	357	16	US-10-618-281-43

12	70.3	1232	16	US-10-618-281-41	Sequence 41, Appl
13	70.3	1259	16	US-10-408-765A-2574	Sequence 2574, Ap
14	64.9	10	17	US-10-663-215-3	Sequence 3, Appl
15	63.5	209	16	US-10-425-115-235061	Sequence 235061,
16	62.2	10	17	US-10-663-215-17	Sequence 17, Appl
17	60.8	9	17	US-10-663-215-22	Sequence 22, Appl
18	59.5	107	15	US-10-424-599-280986	Sequence 280986,
19	59.5	153	16	US-10-425-115-255095	Sequence 255095,
20	59.5	389	15	US-10-424-599-178722	Sequence 178722,
21	59.5	779	15	US-10-389-566-808	Sequence 808, App
22	59.5	1060	15	US-10-389-566-809	Sequence 809, App
23	58.1	10	17	US-10-663-215-15	Sequence 15, Appl
24	56.8	10	17	US-10-663-215-10	Sequence 10, Appl
25	56.8	10	17	US-10-663-215-14	Sequence 14, Appl
26	56.8	14	17	US-10-663-215-6	Sequence 6, Appl
27	56.8	171	15	US-10-425-114-40409	Sequence 40409, A
28	56.8	316	15	US-10-389-566-471	Sequence 471, App
29	56.8	316	16	US-10-739-930-7682	Sequence 7682, Ap
30	56.8	318	15	US-10-389-566-732	Sequence 732, App
31	56.8	318	15	US-10-389-566-2292	Sequence 2292, Ap
32	56.8	318	17	US-10-732-923-23007	Sequence 23007, A
33	56.8	338	15	US-10-389-566-701	Sequence 701, App
34	56.8	395	15	US-10-424-599-191315	Sequence 191315,
35	55.4	296	15	US-10-310-154-708	Sequence 708, App
36	55.4	296	17	US-10-732-923-673	Sequence 673, App
37	54.7	297	16	US-10-767-701-38852	Sequence 38852, A
38	54.7	241	15	US-10-282-122A-58785	Sequence 58785, A
39	54.7	241	15	US-10-335-977-9497	Sequence 9497, Ap
40	54.7	241	15	US-10-335-977-9498	Sequence 9498, Ap
41	54.1	10	17	US-10-663-215-13	Sequence 13, Appl
42	54.1	59	16	US-10-425-115-195824	Sequence 195824,
43	54.1	1427	9	US-09-801-368-354	Sequence 354, App
44	52.7	10	17	US-10-663-215-9	Sequence 9, Appl
45	52.7	121	16	US-10-425-115-294197	Sequence 294197,

ALIGNMENTS

RESULT 1

US-10-663-215-5
; Sequence 5, Application US/10663215
; Publication NO. US20050059588A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Irwin
; APPLICANT: Winograd, Enrique
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Peptides Which Generate Antibodies Resulting in Lysis
; FILE OF INVENTION: of Pathologically Adherent Erythrocytes
; FILE REFERENCE: 023070-140500US
; CURRENT APPLICATION NUMBER: US/10/663,215
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: preferred
; OTHER INFORMATION: native AEI sequence, peptide including two
; OTHER INFORMATION: residues on either side of predicted alpha-helix
US-10-663-215-5

Query Match 100.0%; Score 74; DB 17; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YETFSKLIKIFQDH 14

Db 1 YETFSKLIKIFQDH 14

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RESULT 2
US-10-066-320-2
; Sequence 2, Application US/10066320
; Publication No. US20030022267A1
; GENERAL INFORMATION:
; APPLICANT: Stamler, Jonathan S.
; APPLICANT: Gow, Andrew J.
; APPLICANT: Singel, David J.
; TITLE OF INVENTION: Method for Determining Physiological
; TITLE OF INVENTION: Effects of Hemoglobin
; FILE REFERENCE: 1818.1030-003
; CURRENT APPLICATION NUMBER: US/10/066,320
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US00/21101
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US60/146,680
; PRIOR FILING DATE: 1999-08-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-066-320-2

Query Match      100.0%; Score 74; DB 14; Length 911;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YETFSKLKIFQDH 14
| | | | | | | | | | | | | | | |
Db 534 YETFSKLKIFQDH 547

RESULT 3
US-10-087-464-6
; Sequence 6, Application US/10087464
; Publication No. US20030059436A1
; GENERAL INFORMATION:
; APPLICANT: Chishti, Athar
; APPLICANT: Oh, Steven
; APPLICANT: Liu, David
; APPLICANT: Goel, Vikas
; APPLICANT: Li, Xuerong
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
; FILE REFERENCE: S1237/7019
; CURRENT APPLICATION NUMBER: US/10/087,464
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 06/272,930
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-464-6

Query Match      100.0%; Score 74; DB 14; Length 911;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YETFSKLKIFQDH 14
| | | | | | | | | | | | | | | |
Db 534 YETFSKLKIFQDH 547

RESULT 4
US-10-087-464-8
; Sequence 8, Application US/10087464
; Publication No. US20030059436A1
; GENERAL INFORMATION:
; APPLICANT: Chishti, Athar
```

```
; APPLICANT: Oh, Steven
; APPLICANT: Liu, David
; APPLICANT: Goel, Vikas
; APPLICANT: Li, Xuerong
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
; FILE REFERENCE: S1237/7019
; CURRENT APPLICATION NUMBER: US/10/087,464
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 06/272,930
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-464-8

Query Match      100.0%; Score 74; DB 14; Length 911;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YETFSKLKIFQDH 14
| | | | | | | | | | | | | | | |
Db 534 YETFSKLKIFQDH 547

RESULT 5
US-10-408-765A-3
; Sequence 3, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-3

Query Match      100.0%; Score 74; DB 16; Length 911;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YETFSKLKIFQDH 14
| | | | | | | | | | | | | | | |
Db 534 YETFSKLKIFQDH 547

RESULT 6
US-10-408-765A-500
; Sequence 500, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
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OM protein - protein search, using sw model

Run on: August 26, 2005, 15:47:16 ; Search time 159 Seconds
(without alignments)
34.054 Million cell updates/sec

Title: US-10-663-215-5

Perfect score: 14

Sequence: 1 YETFSKLKIFQDH 14

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 343861

Minimum DB seq length: 14

Maximum DB seq length: 40

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	71.4	17	2 AAW18597	Aaw18597 Aged band
2	9	64.3	15	4 AAB74851	Aab74851 Band 3 pr
3	8	57.1	16	2 AAW18601	Aaw18601 Aged band
4	7	50.0	15	2 AAW01065	Aaw01065 Anion tra
5	5	35.7	16	2 AAY20803	Aay20803 Human neu
6	5	35.7	18	7 ADC29662	Adc29662 Antioxi
7	5	35.7	18	7 ADC29658	Adc29658 Antioxi
8	5	35.7	18	7 ADC29661	Adc29661 Antioxi
9	5	35.7	18	7 ADC29657	Adc29657 Antioxi
10	5	35.7	18	7 ADC29659	Adc29659 Antioxi
11	5	35.7	18	7 ADC29660	Adc29660 Antioxi
12	5	35.7	18	8 ADN16186	Adn16186 AB loop o
13	5	35.7	20	2 AAR28499	Aar28499 Sequence
14	5	35.7	20	2 AAW35627	Aaw35627 Immunomod
15	5	35.7	26	8 ADG75452	Adg75452 Human HLL
16	5	35.7	30	7 ADC29669	Adc29669 Antioxi
17	5	35.7	30	7 ADC29665	Adc29665 Antioxi
18	5	35.7	30	7 ADC29668	Adc29668 Antioxi
19	5	35.7	30	7 ADC29670	Adc29670 Antioxi
20	5	35.7	30	7 ADC29664	Adc29664 Antioxi
21	5	35.7	30	7 ADC29667	Adc29667 Antioxi
22	5	35.7	30	7 ADC29666	Adc29666 Antioxi
23	5	35.7	32	4 AAM18785	Aam18785 Peptide #
24	5	35.7	32	4 ABB37865	Abb37865 Peptide #
25	5	35.7	32	4 AAM31272	Aam31272 Peptide #

RESULT 1

AAW18597	ID	AAW18597	standard; peptide; 17 AA.
XX	AC	AAW18597;	
XX	DT	04-MAR-1998	(first entry)
XX	DE	Aged band 3 peptide (residues 538-554)	epitope IV.
XX	DE	Band 3 protein; antibody; aging antigenic site; Alzheimer's disease;	
XX	KW	phosphorylation; detection; epitope.	
XX	OS	Homo sapiens.	
XX	PN	WO9726537-A1.	
XX	PD	24-JUL-1997.	
XX	PF	13-DEC-1996;	96WO-US020465.
XX	PR	19-JAN-1996;	96US-0010250P.
XX	PA	(RESE) RESEARCH CORP TECHNOLOGIES INC.	
XX	PI	Kay MMB;	
XX	DR	WPI; 1997-385478/35.	
XX	PT	Detecting Alzheimer's disease using antibody that recognises aged band 3	
XX	PT	protein in tissues - or from reduced degree of band 3 protein	
XX	PT	phosphorylation, can be applied to blood or brain samples.	
XX	PS	Claim 10; Page 10; 45pp; English.	
XX	CC	This is an aging antigenic band 3 peptide (residues 538-554) to which a	
XX	CC	specific antibody can bind to. Band 3 is a ubiquitous anion-exchange	
XX	CC	protein and ages as cells and tissues age. Antibodies have been developed	
XX	CC	against this aged band 3. These antibodies bind to distinct regions of	
XX	CC	band 3 in old cells (aging antigenic sites) but not middle aged or young	
XX	CC	cells. This can be used for detecting Alzheimer's disease. A tissue	
XX	CC	sample containing band 3 from a patient suspected of having Alzheimer's	
XX	CC	disease is treated with an antibody that can differentiate between the	
XX	CC	Alzheimer's (aged) and normal band 3, under complex-forming conditions	
XX	CC	and detecting any complex formed. A tissue containing band 3 from a	
XX	CC	healthy control is treated in a similar manner and the amounts of complex	
XX	CC	formed are compared. A significantly greater formation of complex in the	
XX	CC	suspect sample as compared with that of the control is indicative of	

ALIGNMENTS

26	5	35.7	32	4	ABB23124	Abb23124 Protein #
27	5	35.7	32	4	AAM70994	Aam70994 Human bon
28	5	35.7	32	4	AAM58496	Aam58496 Human bra
29	5	35.7	32	4	ABG52711	Abg52711 Human liv
30	5	35.7	32	5	ABG40784	Abg40784 Human pep
31	5	35.7	39	4	AAM96316	Aam96316 Human rep
32	4	28.6	14	2	AAR76352	Aar76352 Bacterial
33	4	28.6	14	2	AAW07925	Aaw07925 gp41 pept
34	4	28.6	14	3	AAB26709	Aab26709 ATM kinase
35	4	28.6	14	4	AAB45779	Aab45779 Human p53
36	4	28.6	14	4	AAB45778	Aab45778 Human SNP
37	4	28.6	14	4	AAG98197	Aag98197 Human SNP
38	4	28.6	14	5	ABB05528	Abb05528 Biotinyia
39	4	28.6	14	5	AAU97487	Aau97487 HIV-1 inf
40	4	28.6	14	8	ADH35703	Adh35703 Apolipop
41	4	28.6	14	8	ADH35732	Adh35732 Apolipop
42	4	28.6	14	8	ADG75469	Adg75469 Human HLL
43	4	28.6	14	8	ADM18975	Adm18975 HLA-DR bo
44	4	28.6	14	8	ADS13340	Ads13340 Human rhe
45	4	28.6	15	2	AAR46993	Aar46993 Apolipop

CC Alzheimer's disease. The disease can also be detected by comparing the
 CC degrees of phosphorylation of band 3 or its degradation products in
 CC suspect and control samples. A significant decrease in phosphorylation in
 CC the suspect sample indicates Alzheimer's disease
 XX
 XX SQ Sequence 17 AA;

Query Match 71.4%; Score 10; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.0014; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SKLIKIFQDH 14
 |||||
 Db 1 SKLIKIFQDH 10

RESULT 2
 AAB74851
 ID AAB74851 standard; peptide; 15 AA.

AC AAB74851;
 DT 19-JUN-2001 (first entry)

XX Band 3 protein-ligand interaction inhibitor peptide SEQ ID NO:8.

XX Anti-plasmodium falciparum; interaction inhibitor; band 3 protein;
 KW thrombolysis; thrombolytic; fibrinolytic; acute myocardial infarction;
 KW lysis; ventricular function; congestive heart failure; mortality;
 KW acute arterial thrombosis; embolism; thrombosis; cerebral sinus.

XX Synthetic.

XX US6191103-B1.

XX 20-FEB-2001.

XX 05-DEC-1997; 97US-00985499.

XX 05-DEC-1997; 97US-00985499.

XX (REGC) UNIV CALIFORNIA.
 XX (BLOO-) CENT BLOOD RES.

XX Shohet SB, Sherman I, Von Andrian U;

XX WPI; 2001-307101/32.

XX Enhancing thrombolysis in mammals comprises administering an inhibitor of
 PT protein band 3-ligand interaction.

XX Claim 28; Col 42; 23pp; English.

XX The present invention describes a method for enhancing thrombolysis in a
 CC mammal. The method comprises the administration to the mammal an amount
 CC of an inhibitor (I) of protein band 3-ligand interaction sufficient to
 CC enhance thrombolysis. (I) has thrombolytic activity. The method is useful
 CC for enhancing thrombolysis in a mammal. (I) is useful for enhancing
 CC fibrinolytic or thrombolytic activity, in the management of acute
 CC myocardial infarction, for lysis of intracoronary thrombi, for
 CC improvement of ventricular function, for reduction of congestive heart
 CC failure, for reduction of mortality, for the lysis of pulmonary emboli
 CC blocking blood flow to one or more lobes of the lung, for the lysis of
 CC acute arterial thrombosis and embolism, for the lysis of thrombosis in
 CC deep veins or in cerebral sinuses, to reopen i.v. catheters obstructed by
 CC clotted blood or fibrin, to prevent clot formation of lysing clots, to
 CC prevent clotting in blood samples drawn from patients for clinical
 CC testing and to prevent the recurrence of thrombosis in patients by
 CC prophylactic administration. The present sequence represents a band 3
 CC protein-ligand interaction inhibitor peptide, which is used in the
 CC exemplification of the present invention
 XX

XX Sequence 15 AA;

Query Match 64.3%; Score 9; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.013; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLKIFQDH 14
 |||||
 Db 1 KLKIFQDH 9

RESULT 3
 AAW18601
 ID AAW18601 standard; peptide; 16 AA.

AC AAW18601;

XX 04-MAR-1998 (first entry)

XX Aged band 3 peptide (residues 526-541) epitope.

XX Band 3 protein; antibody; aging antigenic site; Alzheimer's disease;
 KW phosphorylation; detection; epitope.

XX Homo sapiens.

XX WO9726537-A1.

XX 24-JUL-1997.

XX 13-DEC-1996; 96WO-US020465.

XX 19-JAN-1996; 96US-0010250P.

XX (RESE) RESEARCH CORP TECHNOLOGIES INC.

XX Kay MMB;

XX WPI; 1997-385478/35.

XX Detecting Alzheimer's disease using antibody that recognises aged band 3
 PT protein in tissues - or from reduced degree of band 3 protein
 PT phosphorylation, can be applied to blood or brain samples.

XX Disclosure; Page 11; 45pp; English.

XX This is an aging antigenic band 3 peptide (residues 526-541) to which a
 CC specific antibody can bind to. Band 3 is a ubiquitous anion-exchange
 CC protein and ages as cells and tissues age. Antibodies have been developed
 CC against this aged band 3. These antibodies bind to distinct regions of
 CC band 3 in old cells (aging antigenic sites) but not middle aged or young
 CC cells. This can be used for detecting Alzheimer's disease. A tissue
 CC sample containing band 3 from a patient suspected of having Alzheimer's
 CC disease is treated with an antibody that can differentiate between the
 CC Alzheimer's (aged) and normal band 3, under complex-forming conditions
 CC and detecting any complex formed. A tissue containing band 3 from a
 CC healthy control is treated in a similar manner and the amounts of complex
 CC formed are compared. A significantly greater formation of complex in the
 CC suspect sample as compared with that of the control is indicative of
 CC Alzheimer's disease. The disease can also be detected by comparing the
 CC degrees of phosphorylation of band 3 or its degradation products in
 CC suspect and control samples. A significant decrease in phosphorylation in
 CC the suspect sample indicates Alzheimer's disease

XX Sequence 16 AA;

Query Match 57.1%; Score 8; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YETFSKLI 8
 |||||
 Db 9 YETFSKLI 16

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2005, 15:50:52 ; Search time 39 Seconds
(without alignments)
34.539 Million cell updates/sec

Title: US-10-663-215-5

Perfect score: 14

Sequence: 1 YETFSKLKIFQDH 14

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 7379

Minimum DB seq length: 14

Maximum DB seq length: 40

Post-processing: Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	28.6	15	2 PH0782	T-cell receptor al
2	4	28.6	20	2 C49753	hypothetical prote
3	4	28.6	23	2 S51188	aldenhyde dehydrog
4	4	28.6	28	2 S15235	hypothetical prote
5	4	28.6	34	2 F81044	hypothetical prote
6	4	28.6	35	2 C70229	hypothetical prote
7	4	28.6	35	2 A60496	12K serum protein,
8	4	28.6	36	2 S72299	ribosomal protein,
9	4	28.6	37	2 G71351	probable ribosomal
10	4	28.6	37	2 A82439	hypothetical prote
11	4	28.6	39	2 H81081	hypothetical prote
12	4	28.6	39	2 F97313	hypothetical prote
13	4	28.6	39	2 G85937	hypothetical prote
14	4	28.6	40	2 S20773	Ig heavy chain V r
15	4	28.6	40	2 S09481	hypothetical prote
16	4	28.6	40	2 T07196	hypothetical prote
17	3	21.4	14	2 B29743	translation initia
18	3	21.4	14	2 PH1763	T cell receptor al
19	3	21.4	14	2 PH0800	T-cell receptor al
20	3	21.4	14	2 PH0801	T-cell receptor al
21	3	21.4	14	2 G33160	H+-transporting tw
22	3	21.4	14	2 A39239	actin 8 - slime mo
23	3	21.4	15	2 PH1762	T cell receptor al
24	3	21.4	15	2 S47367	T-cell antigen rec
25	3	21.4	15	2 S47387	T-cell antigen rec
26	3	21.4	15	2 PH0808	T-cell receptor al
27	3	21.4	15	2 PH0797	T-cell receptor al
28	3	21.4	15	2 S03353	plastocyanin - Mic
29	3	21.4	15	2 PA0110	translation elonga

30 3 21.4 16 2 S34444 blaZ protein - Sta
31 3 21.4 16 2 PS0256 22K protein 4208 -
32 3 21.4 16 2 PH1771 T cell receptor al
33 3 21.4 16 2 S51733 T-cell receptor al
34 3 21.4 16 2 E53284 T-cell receptor be
35 3 21.4 16 2 S35627 uvxK protein - pha
36 3 21.4 16 2 T09741 photosystem I chai
37 3 21.4 16 2 B23692 transcription fact
38 3 21.4 16 2 A36889 leu operon leader
39 3 21.4 16 4 I79565 hypothetical TOL3/
40 3 21.4 17 2 I65274 glutathione S-tran
41 3 21.4 17 2 I46151 histone H2AF - dog
42 3 21.4 17 2 I49593 cystic fibrosis tr
43 3 21.4 17 2 I84733 gene CFRP protein
44 3 21.4 17 2 B28027 protein P4 - curle
45 3 21.4 17 2 PH1789 T cell receptor al

ALIGNMENTS

RESULT 1

PH0782

T-cell receptor alpha chain (H3 V-alpha-10. TA57) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PH0782

R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex-r alleles exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0782

A:Molecule type: mRNA

A:Residues: 1-15 <CAS>

A:Cross-references: EMBL:X60883

A:Experimental source: T lymphocyte

A>Note: the authors translated the codon TTC for residue 6 as Leu

C:Keywords: T-cell receptor

Query Match 28.6%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SKLI 8
DB 10 SKLI 13

RESULT 2

C49753

hypothetical protein (prob 5' region) - Serratia marcescens (fragment)

C:Species: Serratia marcescens

C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004

C:Accession: C49753; S11643

R:Omori, K.; Suzuki, S.I.; Imai, Y.; Komatsubara, S.

J. Gen. Microbiol. 137, 509-517, 1991

A:Title: Analysis of the Serratia marcescens proBA operon and feedback control of proline

A:Reference number: A49753; MUID:91237315; PMID:1851803

A:Accession: C49753

A:Molecule type: DNA

A:Residues: 1-20 <OMO>

A:Cross-references: UNIPROT:P22581; GB:X53086; NID:G47251; PIDN:CAA37253.1; PID:G47252

Query Match 28.6%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLJK 9
DB 14 KLJK 17

RESULT 3
S51188
aldehyde dehydrogenase (NAD) (EC 1.2.1.3), cytosolic - clawed frog (fragment)
N;Alternate names: CTB protein; thyroid hormone-binding protein
C;Species: Xenopus sp. (clawed frog)
C;Date: 19-Mar-1997 #sequence_revision 30-Jan-1998 #text_change 15-Mar-2004
C;Accession: S51188
R;Yamauchi, K.; Tata, J.R.
Eur. J. Biochem. 225, 1105-1112, 1994
A;Title: Purification and characterization of a cytosolic thyroid-hormone-binding protein
A;Reference number: S51188; MUID:95045540; PMID:7957201
A;Accession: S51188
A;Molecule type: protein
A;Residues: 1-23 <YAM>
A;Experimental source: adult; liver
C;Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
C;Keywords: cytosol; liver; NAD; oxidoreductase

Query Match 28.6%; Score 4; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLJK 9
Db 15 KLJK 18
|||||

RESULT 4
S15235
hypothetical protein - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S15235
R;Perry, A.C.F.; Bhriain, N.N.; Brown, N.L.; Rouch, D.A.
Mol. Microbiol. 5, 163-171, 1991
A;Title: Molecular characterization of the gor gene encoding glutathione reductase from
ses.
A;Reference number: S15235; MUID:91194546; PMID:1849605
A;Accession: S15235
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <PER>
A;Cross-references: UNIPROT:P23205; EMBL:X54201; NID:945324; PIDN:CAA38121.1; PID:945325

Query Match 28.6%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YETF 4
Db 22 YETF 25
|||||

RESULT 5
F81044
hypothetical protein NM1778 [imported] - Neisseria meningitidis (strain MC58 serogroup
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: F81044
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Hatt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: F81044
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-34 <TET>
A;Cross-references: UNIPROT:Q9JY24; GB:A5002527; GB:A5002098; NID:97227023; PIDN:AAF4211
A;Experimental source: serogroup B, strain MC58
C;Genetics:

A;Gene: NM1778

Query Match 28.6%; Score 4; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LIKI 10
Db 21 LIKI 24
|||||

RESULT 6
C70229
hypothetical protein BBF11 - Lyme disease spirochete plasmid F/1p28-1
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: C70229
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: C70229
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-35 <KLE>
A;Cross-references: UNIPROT:O51019; GB:AE000794; NID:g2589981; PIDN:AAC66379.1; PID:g268;
A;Experimental source: strain B31
C;Genetics:
A;Genome: plasmid

Query Match 28.6%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LIKI 10
Db 22 LIKI 25
|||||

RESULT 7
A60496
12K serum protein, beta-2-m cross-reactive - chicken (fragment)
C;Species: Gallus gallus (Chicken)
C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 09-Jul-2004
C;Accession: A60496
R;Warr, G.W.
Dev. Comp. Immunol. 14, 247-253, 1990
A;Title: A 12 kDa protein in chicken serum antigenically cross-reactive with, but unrelat
A;Reference number: A60496; MUID:90316337; PMID:2196188
A;Accession: A60496
A;Molecule type: protein
A;Residues: 1-35 <WAR>
A;Cross-references: UNIPROT:O7LZS1
A;Comment: This protein resembles beta-2 microglobulin in its size, its presence in serum
C;Keywords: plasma

Query Match 28.6%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSKL 7
Db 3 FSKL 6
|||||

RESULT 8
S72299
ribosomal protein L36 - Plasmodium falciparum plastid
C;Species: Plasmodium falciparum
C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 09-Jul-2004

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OM protein - protein search, using sw model

Run on: August 26, 2005, 15:50:07 ; Search time 170 Seconds
(without alignments)
42.171 Million cell updates/sec

Title: US-10-663-215-5

Perfect score: 14

Sequence: 1 YETFSKLKIFQDH 14

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 41659

Minimum DB seq length: 14

Maximum DB seq length: 40

Post-processing: Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	28.6	14	2	Q6SE39
2	4	28.6	17	1	EFG_THEAQ
3	4	28.6	19	2	Q9ZTV7
4	4	28.6	19	2	Q905K7
5	4	28.6	20	1	YPRB_SERMA
6	4	28.6	20	2	Q95MJ7
7	4	28.6	20	2	Q95MJ8
8	4	28.6	20	2	Q95MJ9
9	4	28.6	20	2	Q95MK0
10	4	28.6	20	2	Q95MK1
11	4	28.6	20	2	Q95MK2
12	4	28.6	20	2	Q95MK3
13	4	28.6	20	2	Q95MK4
14	4	28.6	20	2	Q95MK5
15	4	28.6	20	2	Q95MK6
16	4	28.6	21	2	Q84IJU0
17	4	28.6	21	2	Q71UM9
18	4	28.6	22	2	Q84IJU1
19	4	28.6	23	2	Q9SC60
20	4	28.6	23	2	Q9PRM0
21	4	28.6	24	2	Q9T2H3
22	4	28.6	25	2	Q40972
23	4	28.6	25	2	Q6UGR7
24	4	28.6	25	2	Q6UGR8
25	4	28.6	25	2	Q77X16
26	4	28.6	25	2	Q9IQO4
27	4	28.6	25	2	Q9IQO6
28	4	28.6	25	2	Q9WRV6
29	4	28.6	25	2	Q9WRV2
30	4	28.6	26	2	Q7RL85
31	4	28.6	26	2	Q8JDL0

32 4 28.6 26 2 Q8JDL5 Q8jdl5 human immun
33 4 28.6 27 2 P82945 P82945 loligo peal
34 4 28.6 28 2 Q8CLV6 Q8clv6 yersinia pe
35 4 28.6 29 2 Q83WY0 Q83wy0 streptomyc
36 4 28.6 30 2 Q86UM9 Q86um9 homo sapien
37 4 28.6 30 2 Q7R8Q9 Q7r8q9 plasmodium
38 4 28.6 30 2 Q84LU3 Q84lu3 ginkgo bilo
39 4 28.6 30 2 Q84LU5 Q84lu5 ginkgo bilo
40 4 28.6 30 2 Q84LU7 Q84lu7 ginkgo bilo
41 4 28.6 30 2 Q84LU8 Q84lu8 ginkgo bilo
42 4 28.6 30 2 Q84LV2 Q84lv2 ginkgo bilo
43 4 28.6 30 2 Q84LV4 Q84lv4 ginkgo bilo
44 4 28.6 30 2 Q84LV7 Q84lv7 ginkgo bilo
45 4 28.6 30 2 Q84LW2 Q84lw2 ginkgo bilo

ALIGNMENTS

RESULT 1
Q6SE39 PRELIMINARY; PRT; 14 AA.
AC Q6SE39;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE AcP53Ea (Fragment).
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14762063; DOI=10.1101/gr.1329204;
RA Halligan D.L., Eyre-Walker A., Andolfatto P., Keightley P.D.;
RT "Patterns of evolutionary constraints in intronic and intergenic DNA of Drosophila."
RL Genome Res. 14:273-279(2004).
DR EMBL; AY459579; AAR23030.1; -.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1590 MW; 9B01DA469D3F1E31 CRC64;

Query Match 28.6%; Score 4; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLIK 9
Db 2 KLIK 5

RESULT 2
EFG_THEAQ STANDARD; PRT; 17 AA.
ID EFG_THEAQ
AC Q01697;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elongation factor G (EF-G) (Fragment).
GN Name=fusa; Synonyms=fus;
OS Thermus aquaticus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=271;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP 00276;
RX MEDLINE=92362620; PubMed=1499561;
RA Voss R.H., Hartmann R.K., Lippmann C., Jahn O., Erdmann V.;
RT "Sequence of the tufa gene encoding elongation factor EF-Tu from Thermus aquaticus and overproduction of the protein in Escherichia

```
RT coli.";
RL Eur. J. Biochem. 207:839-846(1992).
CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
CC the nascent protein chain from the A-site to the P-site of the
CC ribosome.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-G/EF-2 subfamily.
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CC -----
DR EMBL; X66322; CAA46997.1; -.
DR HAMAP; MF 00054; -.
DR InterPro; IPR000795; ProtSyn GTPbind.
DR PROSITE; PS00301; EFACITOR_GTP; PARTIAL.
KW Elongation factor; GTP-binding; Protein biosynthesis.
FT NON_TER 1
SQ SEQUENCE 17 AA; 2094 MW; EA4651EF05F86E1D CRC64;
Query Match 28.6%; Score 4; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 KLIK 9
Db 12 KLIK 15
RESULT 3
Q9ZYV7 ID Q9ZYV7 PRELIMINARY; PRT; 19 AA.
AC Q9ZYV7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome oxidase II (Fragment).
OS Myrmecia forficata.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Formicidae; Myrmecinae; Myrmecini; Myrmecia.
OX NCBI_TaxID=32387;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99152621; PubMed=10028295;
RA Dowton M., Austin A.D.;
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
RT the Hymenoptera.";
RL Mol. Biol. Evol. 16:298-309(1999).
DR EMBL; AF034604; AAC79752.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2370 MW; 25AB99B2B1F53B6B CRC64;
Query Match 28.6%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 IKIF 11
Db 8 IKIF 11
RESULT 4
Q905K7 ID Q905K7 PRELIMINARY; PRT; 19 AA.
Q905K7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21663216; PubMed=11804559; DOI=10.1089/08992202753394745;
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA Ndoundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
RA Ido E., Hayami M., Ichimura H., Parra H.Joseph.;
RT "Genetic subtypes of HIV type 1 based on the vpu/env sequences in the
RT Republic of Congo.";
RL AIDS Res. Hum. Retroviruses 18:79-83(2002).
DR EMBL; AF410437; AAL10215.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2176 MW; 3516A49DA9711856 CRC64;
Query Match 28.6%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 LIKI 10
Db 12 LIKI 15
RESULT 5
YPRB SERMA ID YPRB SERMA STANDARD; PRT; 20 AA.
AC P22581;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in prob 5' region (Fragment).
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sr41.
RX MEDLINE=91237315; PubMed=1851803;
RA Omori K., Suzuki S., Imai Y., Komatsubara S.;
RT "Analysis of the Serratia marcescens proBA operon and feedback control
RT of proline biosynthesis.";
RL J. Gen. Microbiol. 137:509-517(1991).
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CC -----
DR EMBL; D90351; BAA14363.1; -.
DR EMBL; X53086; CAA37253.1; -.
DR PIR; C49753; C49753.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2248 MW; 4DD777735276674 CRC64;
Query Match 28.6%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
```

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AC Q905K7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21663216; PubMed=11804559; DOI=10.1089/08992202753394745;
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA Ndoundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
RA Ido E., Hayami M., Ichimura H., Parra H.Joseph.;
RT "Genetic subtypes of HIV type 1 based on the vpu/env sequences in the
RT Republic of Congo.";
RL AIDS Res. Hum. Retroviruses 18:79-83(2002).
DR EMBL; AF410437; AAL10215.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2176 MW; 3516A49DA9711856 CRC64;
Query Match 28.6%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 LIKI 10
Db 12 LIKI 15
RESULT 5
YPRB SERMA ID YPRB SERMA STANDARD; PRT; 20 AA.
AC P22581;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in prob 5' region (Fragment).
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sr41.
RX MEDLINE=91237315; PubMed=1851803;
RA Omori K., Suzuki S., Imai Y., Komatsubara S.;
RT "Analysis of the Serratia marcescens proBA operon and feedback control
RT of proline biosynthesis.";
RL J. Gen. Microbiol. 137:509-517(1991).
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CC or send an email to license@isb-sib.ch.)
CC -----
DR EMBL; D90351; BAA14363.1; -.
DR EMBL; X53086; CAA37253.1; -.
DR PIR; C49753; C49753.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2248 MW; 4DD777735276674 CRC64;
Query Match 28.6%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2005, 15:51:37 ; Search time 41 Seconds
(without alignments)
25.490 Million cell updates/sec

Title: US-10-663-215-5

Perfect score: 14

Sequence: 1 YETFSKLKIFQDH 14

Scoring table: OLIGO

Gapex 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 118471

Minimum DB seq length: 14

Maximum DB seq length: 40

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/prodata/1/iaa/5A COMB.pcp.*
- 2: /cgn2_6/prodata/1/iaa/5B COMB.pcp.*
- 3: /cgn2_6/prodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/prodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2_6/prodata/1/iaa/6C COMB.pcp.*
- 6: /cgn2_6/prodata/1/iaa/6D COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	64.3	15	3	US-08-985-499-8
2	7	50.0	15	3	US-08-405-647B-8
3	7	50.0	15	5	PCT-US96-03180-8
4	5	35.7	18	4	US-09-389-603-15
5	5	35.7	20	1	US-07-686-116A-3
6	5	35.7	20	1	US-08-614-935-20
7	5	35.7	20	3	US-09-130-287-20
8	5	35.7	31	2	US-08-568-310D-6
9	5	35.7	31	3	US-09-270-455-6
10	5	35.7	31	4	US-08-437-943D-19
11	5	35.7	32	1	US-08-435-925C-17
12	5	35.7	32	1	US-08-435-925C-18
13	5	35.7	36	3	US-08-474-349A-411
14	5	35.7	36	3	US-08-474-349A-412
15	4	28.6	14	1	US-08-218-025A-170
16	4	28.6	14	3	US-08-475-213-7
17	4	28.6	14	3	US-09-400-653A-7
18	4	28.6	14	3	US-09-248-061B-7
19	4	28.6	14	4	US-09-695-437A-26
20	4	28.6	15	1	US-08-311-611A-113
21	4	28.6	15	1	US-08-372-783-113
22	4	28.6	15	1	US-08-372-105-113
23	4	28.6	15	1	US-08-306-473A-113
24	4	28.6	15	1	US-08-277-660A-1
25	4	28.6	15	1	US-08-277-660A-4
26	4	28.6	15	1	US-08-277-660A-5
27	4	28.6	15	1	US-08-424-957-1

28 4 28.6 15 1 US-08-424-957-20 Sequence 20, Appl
29 4 28.6 15 1 US-08-424-957-21 Sequence 21, Appl
30 4 28.6 15 1 US-08-480-190-228 Sequence 228, Appl
31 4 28.6 15 2 US-08-621-803-97 Sequence 97, Appl
32 4 28.6 15 2 US-08-485-445A-113 Sequence 113, Appl
33 4 28.6 15 2 US-08-637-759B-45 Sequence 45, Appl
34 4 28.6 15 2 US-08-488-379-228 Sequence 228, Appl
35 4 28.6 15 3 US-08-871-355A-45 Sequence 45, Appl
36 4 28.6 15 3 US-08-660-347-3 Sequence 3, Appl
37 4 28.6 15 3 US-09-119-263-113 Sequence 113, Appl
38 4 28.6 15 3 US-08-834-314-3 Sequence 113, Appl
39 4 28.6 15 3 US-08-657-162-113 Sequence 113, Appl
40 4 28.6 15 3 US-09-035-686-1 Sequence 1, Appl
41 4 28.6 15 3 US-09-035-686-20 Sequence 20, Appl
42 4 28.6 15 3 US-09-035-686-21 Sequence 21, Appl
43 4 28.6 15 3 US-09-224-480-113 Sequence 113, Appl
44 4 28.6 15 3 US-09-217-352-97 Sequence 97, Appl
45 4 28.6 15 3 US-09-201-945-45 Sequence 45, Appl

ALIGNMENTS

RESULT 1

US-08-985-499-8
; Sequence 8, Application US/08985499
; Patent No. 6191103
; GENERAL INFORMATION:
; APPLICANT: Shohet, Stephen B.
; APPLICANT: Sherman, Irwin
; APPLICANT: von Andrian, Ulrich
; TITLE OF INVENTION: Methods for Enhancing Thrombolysis in a
; TITLE OF INVENTION: Manual
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,499
; FILING DATE: 05-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hyman, Laurence J.
; REGISTRATION NUMBER: 35,551
; REFERENCE/DOCKET NUMBER: 02307E-084500US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-985-499-8

Query Match 64.3%; Score 9; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKIFQDH 14

DB 1 KLKIFQDH 9

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RESULT 2
US-08-405-647B-8
; Sequence 8, Application US/08405647B
; Patent No. 6124262
; GENERAL INFORMATION:
; APPLICANT: Sherman, Irwin W.
; APPLICANT: Crandall, Ian E.
; APPLICANT: Thevenin, Bernard Jean-Marie
; TITLE OF INVENTION: Compositions and Methods for Reducing
; TITLE OF INVENTION: Adhesiveness of Defective Red Blood Cells
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,647B
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 02307E-068700US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-405-647B-8

Query Match 50.0%; Score 7; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLIKIFQ 12
Db 1 KLIKIFQ 7

RESULT 3
PCT-US96-03180-8
; Sequence 8, Application PC/TUS9603180
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University
; APPLICANT: of California
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REDUCING
; TITLE OF INVENTION: ADHESIVENESS OF DEFECTIVE RED BLOOD CELLS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 North Figueroa Street, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/03180
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-370
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US96-03180-8

Query Match 50.0%; Score 7; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLIKIFQ 12
Db 1 KLIKIFQ 7

RESULT 4
US-09-389-603-15
; Sequence 15, Application US/09389603
; Patent No. 6737234
; GENERAL INFORMATION:
; APPLICANT: Freimuth, Paul I
; APPLICANT: Flanagan, John M.
; APPLICANT: Bewley, Maria C.
; TITLE OF INVENTION: STRUCTURE OF ADENOVIRUS BOUND TO CELLULAR RECEPTOR CAR
; FILE REFERENCE: CIP OF BNL2007
; CURRENT APPLICATION NUMBER: US/09/389,603
; CURRENT FILING DATE: 1999-09-03
; EARLIER APPLICATION NUMBER: 09/236,423
; EARLIER FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Adenovirus type 40 short
US-09-389-603-15

Query Match 35.7%; Score 5; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YETFS 5
Db 14 YETFS 18

RESULT 5
US-07-686-116A-3
; Sequence 3, Application US/07686116A
; Patent No. 5225399
; GENERAL INFORMATION:
; APPLICANT: Kari, U. Prasad
; APPLICANT: Maloy, W. Lee
; APPLICANT: Zaslloff, Michael
; TITLE OF INVENTION: No. 5225399el Biologically Active Peptide
; TITLE OF INVENTION: Compositions and Uses Therefor
; NUMBER OF SEQUENCES: 6
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2005, 15:54:28 ; Search time 158 Seconds
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34.816 Million cell updates/sec

Title: US-10-663-215-5
Perfect score: 14
Sequence: 1 YETFSKLIKIFODH 14

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Gapop 60.0 , Gapext 60.0

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Total number of hits satisfying chosen parameters: 194914

Minimum DB seq length: 14
Maximum DB seq length: 40

Post-processing: Listing first 45 summaries

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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	14	100.0	14	17	US-10-663-215-5
2	5	35.7	14	17	US-10-874-923-194
3	5	35.7	15	17	US-10-874-923-182
4	5	35.7	16	17	US-10-808-187-2107
5	5	35.7	16	18	US-10-807-807-2107
6	5	35.7	18	14	US-10-142-238A-32
7	5	35.7	18	14	US-10-142-238A-33
8	5	35.7	18	14	US-10-142-238A-34
9	5	35.7	18	14	US-10-142-238A-35
10	5	35.7	18	14	US-10-142-238A-36
11	5	35.7	18	14	US-10-142-238A-37

12	5	35.7	22	15	US-10-465-789A-49	Sequence 49, Appl
13	5	35.7	22	20	US-11-033-489-49	Sequence 49, Appl
14	5	35.7	26	14	US-10-271-078-13	Sequence 13, Appl
15	5	35.7	27	16	US-10-425-115-216756	Sequence 216756,
16	5	35.7	30	14	US-10-142-238A-39	Sequence 39, Appl
17	5	35.7	30	14	US-10-142-238A-40	Sequence 40, Appl
18	5	35.7	30	14	US-10-142-238A-41	Sequence 41, Appl
19	5	35.7	30	14	US-10-142-238A-42	Sequence 42, Appl
20	5	35.7	30	14	US-10-142-238A-43	Sequence 43, Appl
21	5	35.7	30	14	US-10-142-238A-44	Sequence 44, Appl
22	5	35.7	30	14	US-10-142-238A-45	Sequence 45, Appl
23	5	35.7	31	8	US-08-438-182-19	Sequence 19, Appl
24	5	35.7	32	9	US-09-864-761-38422	Sequence 38422, A
25	5	35.7	32	16	US-10-437-963-194326	Sequence 194326,
26	5	35.7	36	16	US-10-437-963-182166	Sequence 182166,
27	5	35.7	38	16	US-10-437-963-145708	Sequence 145708,
28	5	35.7	39	10	US-09-764-891-4974	Sequence 4974, Ap
29	5	35.7	39	15	US-10-424-599-216523	Sequence 216523,
30	5	35.7	40	16	US-10-425-115-296865	Sequence 296865,
31	4	28.6	40	14	US-10-024-123-7	Sequence 7, Appli
32	4	28.6	41	14	US-10-271-078-30	Sequence 30, Appl
33	4	28.6	41	14	US-10-601-100-43	Sequence 43, Appl
34	4	28.6	41	15	US-10-275-427A-13	Sequence 13, Appl
35	4	28.6	41	15	US-10-676-909-10	Sequence 10, Appl
36	4	28.6	41	16	US-10-865-478-839	Sequence 839, App
37	4	28.6	41	17	US-10-874-923-16	Sequence 16, Appl
38	4	28.6	41	17	US-10-874-923-36	Sequence 36, Appl
39	4	28.6	41	17	US-10-874-923-137	Sequence 137, App
40	4	28.6	41	17	US-10-874-923-218	Sequence 218, App
41	4	28.6	41	17	US-10-801-990-131	Sequence 131, App
42	4	28.6	41	18	US-10-862-195-820	Sequence 620, App
43	4	28.6	41	15	US-09-765-527-97	Sequence 97, Appl
44	4	28.6	41	15	US-09-732-384-6	Sequence 6, Appli
45	4	28.6	41	15	US-09-818-564-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-663-215-5
; Sequence 5, Application US/10663215
; Publication NO. US20050059588A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Irwin
; APPLICANT: Winograd, Enrique
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Peptides Which Generate Antibodies Resulting in Lysis
; FILE REFERENCE: 023070-140500US
; CURRENT APPLICATION NUMBER: US/10/663,215
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:preferred
; OTHER INFORMATION: native AEI sequence, peptide including two
; OTHER INFORMATION: residues on either side of predicted alpha-helix

Query Match 100.0%; Score 14; DB 17; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YETFSKLIKIFODH 14
DB 1 YETFSKLIKIFODH 14

RESULT 2
US-10-874-923-194
; Sequence 194, Application US/10874923
; Publication No. US20050032166A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ADIPONECTIN RECEPTOR VARIANTS
; FILE REFERENCE: D0338 NP
; CURRENT APPLICATION NUMBER: US/10/874,923
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: U.S. 60/482,324
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: U.S. 60/486,036
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: U.S. 60/492,470
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: U.S. 60/508,225
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: U.S. 60/552,084
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 194
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-874-923-194

Query Match 35.7%; Score 5; DB 17; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TFSKL 7
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Db 4 TFSKL 8

RESULT 3
US-10-874-923-182
; Sequence 182, Application US/10874923
; Publication No. US20050032166A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ADIPONECTIN RECEPTOR VARIANTS
; FILE REFERENCE: D0338 NP
; CURRENT APPLICATION NUMBER: US/10/874,923
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: U.S. 60/482,324
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: U.S. 60/486,036
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: U.S. 60/492,470
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: U.S. 60/508,225
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: U.S. 60/552,084
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 182
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-874-923-182

Query Match 35.7%; Score 5; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TFSKL 7
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Db 11 TFSKL 15

RESULT 4
US-10-808-187-2107
; Sequence 2107, Application US/10808187
; Publication No. US20050090909A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 2107
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-2107

Query Match 35.7%; Score 5; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TFSKL 7
| | | | |
Db 2 TFSKL 6

RESULT 5
US-10-807-807-2107
; Sequence 2107, Application US/10807807
; Publication No. US20050181357A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, FREDERICK C.
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
; FILE REFERENCE: V9661.0077
; CURRENT APPLICATION NUMBER: US/10/807,807
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2005, 16:08:10 ; Search time 174 Seconds
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41.202 Million cell updates/sec

Title: US-10-663-215-6

Perfect score: 50

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	46	92.0	905	2 Q7ZZJ7	Q7zzj7 brachydanio
8	44	88.0	308	2 Q98FW2	Q98fw2 rhizobium l
9	44	88.0	466	2 Q99LT5	Q99lt5 mus musculu
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13	44	88.0	1237	2 Q7TPS4	Q7tps4 mus musculu
14	43	86.0	81	2 Q9TRC8	Q9trc8 bos taurus
15	43	86.0	147	2 Q9GKN5	Q9gkn5 bos taurus
16	43	86.0	622	2 Q9TU75	Q9tu75 sus scrofa
17	43	86.0	663	2 Q9TUQ1	Q9tuq1 bos taurus
18	43	86.0	855	2 Q9TUQ0	Q9tuq0 bos taurus
19	43	86.0	922	1 B3AT CHICK	P15575 gallus gall
20	43	86.0	930	2 Q9XSW5	Q9xsw5 bos taurus
21	43	86.0	1087	2 Q6PUJ3	Q6puj3 homo sapien
22	43	86.0	1159	2 Q8TAG3	O8tag3 homo sapien
23	43	86.0	1227	2 Q9UEY4	Q9uey4 homo sapien
24	43	86.0	1232	2 Q9UEY5	Q9uey5 homo sapien
25	43	86.0	1237	2 Q6SJF2	Q6sjf2 equus cabal
26	43	86.0	1238	1 B3A2_CAVPO	Q92088 cavia porce
27	43	86.0	1241	1 B3A2_HUMAN	P04920 homo sapien
28	43	86.0	1241	2 Q996E4	Q996e4 homo sapien
29	43	86.0	1241	2 Q9UEY6	Q9uey6 homo sapien
30	43	86.0	3167	2 Q7QQ87	Q7qq87 giardia lam
31	42	84.0	1219	2 Q90710	Q90710 gallus gall

32 41 82.0 196 2 Q953B8 Q953B8 kikirhia nel
33 40 80.0 55 2 Q64CG1 Q64cgl uncultured
34 40 80.0 197 2 Q953A5 Q953a5 kikirhia scu
35 40 80.0 212 2 Q70TD5 Q70td5 folevella f
36 40 80.0 293 2 Q35403 Q35403 mus musculu
37 40 80.0 316 2 Q9EP86 Q9ep86 mus musculu
38 40 80.0 664 1 MS16_YEAST P15424 saccharomyc
39 40 80.0 844 2 Q90579 Q90579 gallus gall
40 40 80.0 1547 2 Q7QV96 Q7qv96 giardia lam
41 39 78.0 132 2 Q956K5 Q956k5 rhodotorula
42 39 78.0 132 2 Q7Y7Y8 Q7y7y8 rhizopus mi
43 39 78.0 191 2 Q953B7 Q953b7 kikirhia sub
44 39 78.0 192 2 Q953A4 Q953a4 kikirhia cau
45 39 78.0 193 2 Q953B0 Q953b0 kikirhia cut

ALIGNMENTS

RESULT 1

Q91ZE7 PRELIMINARY; PRT; 849 AA.
AC Q91ZE7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Band 3 anion exchange protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Ye H., Binder H.J., Rajendran V.M.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY030082; AAK38733.1; -
DR HSSP; P02730; 1ETS.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005452; F:inorganic anion exchanger activity; IEA.
DR GO; GO:0006820; P:anion transport; IEA.
DR Pfam; PF07585; Band_3_cyto; 1.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR00165; ANIONEXCHNGR.
DR PRINTS; PR01187; ANIONEXHNGR1.
DR PRINTS; PR01231; HCO3TRNSPORT.
DR TIGRfam; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SQ SEQUENCE 849 AA; 94312 MW; 84B200780CB07D3A CRC64;

Query Match 100.0%; Score 50; DB 2; Length 849;

Best Local Similarity 64.3%; Pred. No. 8.1;

Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YXTFSLXIXFQXX 14

Db 473 YETFSKLIFQDY 486

RESULT 2

B3AT HUMAN STANDARD; PRT; 911 AA.
ID B3AT HUMAN
AC P02730;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
DE (CD233 antigen).
GN Name=SLC4A1; Synonyms=AE1, DI, EPB3;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90083213; PubMed=2594752;
RA Lux S.E., John K.M., Kopito R.R., Lodish H.F.;
RT "Cloning and characterization of band 3, the human erythrocyte anion-
RT exchange protein (AE1).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:9089-9093(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=89134172; PubMed=3223947;
RA Tanner M.J.A., Martin P.G., High S.;
RT "The complete amino acid sequence of the human erythrocyte membrane
RT anion-transport protein deduced from the cDNA sequence.";
RL Biochem. J. 256:703-712(1988).
RN [3]
RP SEQUENCE OF 1-199; 220-292 AND 347-370.
RX MEDLINE=90001294; PubMed=2790053; DOI=10.1016/0167-4838(89)90116-7;
RA Yannoukakos D., Vasseur C., Blouquit Y., Bursaux E., Wajzman H.;
RT "Primary structure of the cytoplasmic domain of human erythrocyte
RT protein band 3. Comparison with its sequence in the mouse.";
RL Biochim. Biophys. Acta 998:43-49(1989).
RN [4]
RP SEQUENCE OF 1-201.
RX MEDLINE=83238395; PubMed=6345535;
RA Kaul R.K., Murthy S.N.P., Reddy A.G., Steck T.L., Kohler H.;
RT "Amino acid sequence of the N alpha-terminal 201 residues of human
RT erythrocyte membrane band 3.";
RL J. Biol. Chem. 258:7981-7990(1983).
RN [5]
RP SEQUENCE OF 1-3.
RX MEDLINE=79027186; PubMed=701248;
RA Drickamer L.K.;
RT "Orientation of the band 3 polypeptide from human erythrocyte
RT membranes. Identification of NH2-terminal sequence and site of
RT carbohydrate attachment.";
RL J. Biol. Chem. 253:7242-7248(1978).
RN [6]
RP SEQUENCE OF 559-630.
RX MEDLINE=83308584; PubMed=6615451;
RA Brock C.J., Tanner M.J.A., Kemp C.;
RT "The human erythrocyte anion-transport protein. Partial amino acid
RT sequence, conformation and a possible molecular mechanism for anion
RT exchange.";
RL Biochem. J. 213:577-586(1983).
RN [7]
RP SEQUENCE OF 834-911.
RX MEDLINE=88228050; PubMed=3372523;
RA Kawano Y., Okubo K., Tokunaga F., Miyata T., Iwanaga S., Hamasaki N.;
RT "Localization of the pyridoxal phosphate binding site at the COOH-
RT terminal region of erythrocyte band 3 protein.";
RL J. Biol. Chem. 263:8232-8238(1988).
RN [8]
RP ROLE OF GLU-681, AND SEQUENCE OF 665-688.
RX MEDLINE=9232495; PubMed=1352774;
RA Jennings M.L., Smith J.S.;
RT "Anion-proton cotransport through the human red blood cell band 3
RT protein. Role of glutamate 681.";
RL J. Biol. Chem. 267:13964-13971(1992).
RN [9]
RP PALMITOYLATION OF CYS-843.
RX MEDLINE=91358422; PubMed=1885574;
RA Okubo K., Hamasaki N., Hara K., Kageura M.;
RT "Palmitoylation of cysteine 69 from the COOH-terminal of band 3
RT protein in the human erythrocyte membrane. Acylation occurs in the
RT middle of the consensus sequence of F--I-ITGLAVL found in band 3
RT protein and G2 protein of Rift Valley fever virus.";
RL J. Biol. Chem. 266:16420-16424(1991).
RN [10]
RP PHOSPHORYLATION SITES TYR-8; TYR-21; TYR-359 AND TYR-904.
RX MEDLINE=20400020; PubMed=10942405;
RA Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono E.,
Pinna L.A., Donella-Deana A.;
RT "Sequential phosphorylation of protein band 3 by Syk and Lyn tyrosine
RT kinases in intact human erythrocytes: identification of primary and
RT secondary phosphorylation sites.";
RL Blood 96:1550-1557(2000).
RN [11]
RP VARIANT MEMPHIS GLU-56.
RX MEDLINE=91329825; PubMed=1678289;
RA Yannoukakos D., Vasseur C., Driancourt C., Blouquit Y., Delauney J.,
RA Wajzman H., Bursaux E.;
RT "Human erythrocyte band 3 polymorphism (band 3 Memphis):
RT characterization of the structural modification (Lys 56-->Glu) by
RT protein chemistry methods.";
RL Blood 78:1117-1120(1991).
RN [12]
RP VARIANT HE 400-ALA-408 DEL, AND VARIANT MEMPHIS GLU-56.
RX MEDLINE=92107882; PubMed=1722314;
RA Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T.,
RA Rubin H.L., Zhai S., Sahr K.E., Liu S.-C.;
RT "Deletion in erythrocyte band 3 gene in malaria-resistant Southeast
RT Asian ovalocytosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:11022-11026(1991).
RN [13]
RP VARIANT HS ARG-327.
RX MEDLINE=92329950; PubMed=1378323;
RA Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C.,
RA Cohen C.M.;
RT "Band 3 Tuscaloosa: Pro-327-->Arg substitution in the cytoplasmic
RT domain of erythrocyte band 3 protein associated with spherocytic
RT hemolytic anemia and partial deficiency of protein 4.2.";
RL Blood 80:523-529(1992).
RN [14]
RP VARIANT HE 400-ALA-408 DEL.
RX MEDLINE=92167271; PubMed=1538405;
RA Schofield A.E., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M.,
RA Nash G.B., Dluzewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M.,
RA Gratzner W.B.;
RT "Basis of unique red cell membrane properties in hereditary
RT ovalocytosis.";
RL J. Mol. Biol. 223:949-958(1992).
RN [15]
RP VARIANT HS LEU-868.
RX MEDLINE=93343855; PubMed=8343110;
RA Bruce L.J., Kay M.M., Lawrence C., Tanner M.J.;
RT "Band 3 HT, a human red-cell variant associated with acanthocytosis
RT and increased anion transport, carries the mutation Pro-868-->Leu in
RT the membrane domain of band 3.";
RL Biochem. J. 293:317-320(1993).
RN [16]
RP VARIANT MONTEFIORE LYS-40.
RX MEDLINE=93229758; PubMed=8471774;
RA Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L.,
RA Schwartz R.S.;
RT "Human erythrocyte protein 4.2 deficiency associated with hemolytic
RT anemia and a homozygous 40 glutamic acid-->lysine substitution in the
RT cytoplasmic domain of band 3 (band 3Montefiore).";
RL Blood 81:2155-2165(1993).
RN [17]
RP VARIANT BLOOD GROUP DI(A)/MEMPHIS-II.
RX MEDLINE=94266802; PubMed=8206915;
RA Bruce L.J., Anstee D.J., Spring F.A., Tanner M.J.;
RT "Band 3 Memphis variant II. Altered stilbene disulfonate binding and
RT the Diego (Dia) blood group antigen are associated with the human
RT erythrocyte band 3 mutation Pro-854-->Leu.";
RL J. Biol. Chem. 269:16155-16158(1994).
RN [18]
RP VARIANT BLOOD GROUP WR(A).
RX MEDLINE=95111140; PubMed=7812009;
RA Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson S.,
RA Tanner M.J.;
RT "Changes in the blood group Wright antigens are associated with a
RT mutation at amino acid 658 in human erythrocyte band 3: a site of
RT interaction between band 3 and glycophorin A under certain

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OM protein - protein search, using sw model

Run on: August 26, 2005, 16:05:19 ; Search time 69 Seconds
(without alignments)
78.473 Million cell updates/sec

Title: US-10-663-215-6

Perfect score: 50

Sequence: 1 YXFSXLIXIFQXX 14

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Desc04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	50	100.0	58	2 AAW01093	Aaw01093 Exofacial
2	50	100.0	58	4 AAB74884	Aab74884 Human ban
3	50	100.0	80	4 AAU30823	Aau30823 Novel hum
4	50	100.0	911	2 AAR15355	Aar15355 Human ery
5	50	100.0	911	2 AAW90263	Aaw90263 A. tigrin
6	50	100.0	911	4 AAB46914	Aab46914 Human ery
7	50	100.0	911	5 AAE29343	Aae29343 Human Ban
8	50	100.0	911	5 AAE29344	Aae29344 Human Ban
9	50	100.0	911	7 ADE56706	Ade56706 Human Pro
10	50	100.0	911	7 ADJ68197	Adj68197 Human hea
11	50	100.0	911	7 ADJ68694	Adj68694 Human hea
12	50	100.0	911	8 ADL08510	Adl08510 Human tum
13	50	100.0	927	7 ADE56704	Ade56704 Rat Prote
14	50	100.0	933	8 ABM84084	Abm84084 Human dia
15	50	100.0	962	4 AAU30825	Aau30825 Human cat
16	45	90.0	50	5 ABB84592	Abb84592 Human cat
17	44	88.0	1234	7 ADE56763	Ade56763 Rat Prote
18	44	88.0	1234	7 ADE56753	Ade56753 Rat Prote
19	44	88.0	1234	7 ADE56759	Ade56759 Rat Prote
20	44	88.0	1234	7 ADE56757	Ade56757 Rat Prote
21	44	88.0	1237	8 ADF72495	Adf72495 Osteoclas
22	43	86.0	1227	8 ADF72499	Adf72499 Osteoclas
23	43	86.0	1232	8 ADF72501	Adf72501 Osteoclas
24	43	86.0	1240	7 AAW90262	Aaw90262 A. tigrin
25	43	86.0	1241	7 ADE56755	Ade56755 Human Pro

ALIGNMENTS

RESULT 1

AAW01093

ID AAW01093 standard; peptide; 58 AA.

AC AAW01093;

XX

DT 08-MAY-1997 (first entry)

DE Exofacial region loop 3 of band 3 protein (residues 520-577).

XX

KW Anion transporter band 3 protein; endothelial adhesion; red blood cell;
KW cytoplasmic domain; erythrocyte; exofacial loop; epitope; antibody;
KW mammal; plasmodium falciparum infection; sickle cell disease; diabetes;
KW band 3; thalassemia; anaemia; therapy.

OS Synthetic.

XX WO9629086-A1.

XX 26-SEP-1996.

XX 07-MAR-1996; 96WO-US003180.

XX 17-MAR-1995; 95US-00405647.

XX (REGC) UNIV CALIFORNIA.

XX Sherman IW, Crandall IE, Shohet SB, Thevenin BJ;

XX WPI; 1996-442944/44.

XX Peptide(s) with amino acid motifs in band 3 - used for reducing the adhesiveness of red blood cells for treating malaria, sickle cell disease, thalassemia or diabetes.

XX Example 2; Page 20; 48pp; English.

XX AAW01053-W01095 represent peptides isolated from (or based on) regions of the anion transporter band 3 protein. The band 3 protein is present in a million copies per red blood cell, in the form of monomers, dimers, or tetramers. Band 3 protein has two distinct domains, a 43 kD water-soluble cytoplasmic domain, and a 55 kD membrane spanning domain. In an number of otherwises-unrelated conditions (such as malaria, and diabetes), there are modifications in band 3, such that there is clustering and a change in the conformation of the protein. Due to this change in protein conformation (and by the exposure of cryptic adhesive sites), the normally non-adherent erythrocyte becomes a cell with enhanced endothelial adhesiveness. These sequences were found in the putative

Ade56761 Human Pro
Ade57913 Human Pro
Adf72497 Osteoclas
Adl25374 HCO3-tran
Adn19001 Bacterial
Abu27903 Protein e
Abu31675 Protein e
Abo65978 Klebsiell
Aau83127 Novel sec
Aay37658 Protein w
Aag14057 Arabidops
Aab22969 Streptoco
Abp27445 Streptoco
Aag47141 Arabidops
Abp97646 Amino aci
Abm68596 Photorhab
Abm68916 Photorhab
Abr84489 Mouse ani
Aab18279 Plasmodiu
Aam06341 Human foe

26 43 86.0 1241 7 ADE56761
27 43 86.0 1241 7 ADE57913
28 43 86.0 1241 8 ADF72497
29 41 82.0 713 7 ADL25374
30 40 80.0 664 8 ADN19001
31 39 78.0 217 6 ABU27903
32 39 78.0 217 6 ABU31675
33 39 78.0 221 7 ABO65978
34 39 78.0 419 5 AAU83127
35 37 74.0 163 2 AAY37658
36 37 74.0 188 3 AAG14057
37 37 74.0 308 5 ABP22969
38 37 74.0 328 5 ABP27445
39 37 74.0 338 3 AAG47141
40 37 74.0 354 6 ABP97646
41 37 74.0 414 6 ABM68596
42 37 74.0 519 6 ABM68916
43 37 74.0 790 7 ABR84489
44 37 74.0 885 3 AAB18279
45 36 72.0 57 4 AAM06341

CC exofacial loops of band 3, and are epitopes for antibody binding. These
CC sequences compete with the altered band 3 protein, and thereby block the
CC adhesiveness of the red blood cells. The peptides can be used for
CC reducing the adhesiveness of red blood cells in a mammalian patient
CC characterised by a condition selected from Plasmodium falciparum
CC infection, sickle cell disease, thalassaemia and diabetes
XX SQ Sequence 58 AA;
SQ Query Match 100.0%; Score 50; DB 2; Length 58;
Best Local Similarity 64.3%; Pred. No. 0.31;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YXTFSXLIXIFQXX 14
Db 15 YETFSKLKIFQDH 28
RESULT 2
ID AAB74884 standard; peptide; 58 AA.
XX AC AAB74884;
XX DT 19-JUN-2001 (first entry)
XX DE Human band 3 protein predicted exofacial region loop 3 SEQ ID NO:41.
XX KW Anti-Plasmodium falciparum; interaction inhibitor; band 3 protein;
KW thrombolysis; thrombolytic; fibrinolytic; acute myocardial infarction;
KW lysis; ventricular function; congestive heart failure; mortality;
KW acute arterial thrombosis; embolism; thrombosis; cerebral sinus.
XX OS Homo sapiens.
XX PN US61911103-B1.
XX PD 20-FEB-2001.
XX PF 05-DEC-1997; 97US-00985499.
XX PR 05-DEC-1997; 97US-00985499.
XX PA (REGC) UNIV CALIFORNIA.
XX PA (BLOO-) CENT BLOOD RES.
XX PI Shohet SB, Sherman I, Von Andrian U;
XX WPI; 2001-307101/32.
XX DR Enhancing thrombolysis in mammals comprises administering an inhibitor of
XX PT protein band 3-ligand interaction.
XX PS Disclosure; Col 7; 23pp; English.
XX CC The present invention describes a method for enhancing thrombolysis in a
XX CC mammal. The method comprises the administration to the mammal an amount
XX CC of an inhibitor (I) of protein band 3-ligand interaction sufficient to
XX CC enhance thrombolysis. (I) has thrombolytic activity. The method is useful
XX CC for enhancing thrombolysis in a mammal. (I) is useful for enhancing
XX CC fibrinolytic or thrombolytic activity, in the management of acute
XX CC myocardial infarction, for lysis of intracoronary thrombi, for
XX CC improvement of ventricular function, for reduction of congestive heart
XX CC failure, for reduction of mortality, for the lysis of pulmonary emboli
XX CC blocking blood flow to one or more lobes of the lung, for the lysis of
XX CC acute arterial thrombosis and embolism, for the lysis of thrombosis in
XX CC deep veins or in cerebral sinuses, to reopen i.v. catheters obstructed by
XX CC clotted blood or fibrin, to prevent clot formation of lysing clots, to
XX CC prevent clotting in blood samples drawn from patients for clinical
XX CC testing and to prevent the recurrence of thrombosis in patients by
XX CC prophylactic administration. The present sequence represents a human band
XX CC 3 protein predicted exofacial region loop peptide, which is used in the
XX CC exemplification of the present invention

XX SQ Sequence 58 AA;
SQ Query Match 100.0%; Score 50; DB 4; Length 58;
Best Local Similarity 64.3%; Pred. No. 0.31;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YXTFSXLIXIFQXX 14
Db 15 YETFSKLKIFQDH 28
RESULT 3
ID AAU30823 standard; protein; 80 AA.
XX AC AAU30823;
XX DT 18-DEC-2001 (first entry)
XX DE Novel human secreted protein #1314.
XX KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX OS Homo sapiens.
XX PN WO200179449-A2.
XX PD 25-OCT-2001.
XX PF 16-APR-2001; 2001WO-US008656.
XX PR 18-APR-2000; 2000US-00552929.
XX PR 26-JAN-2001; 2001US-00770160.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-611725/70.
XX DR Nucleic acids encoding a range of human polypeptides, useful in genetic
XX PT vaccination, testing and therapy.
XX PS Claim 20; Page 353; 765pp; English.
XX CC The invention relates to novel human secreted polypeptides. The
XX CC polypeptides and antibodies to the polypeptides are useful for
XX CC determining the presence of or predisposition to a disease associated
XX CC with altered levels of polypeptide. The polypeptides are also useful for
XX CC identifying agents (agonists and antagonists) that bind to them. Cells
XX CC expressing the proteins are useful for identifying a therapeutic agent
XX CC for use in treatment of a pathology related to aberrant expression or
XX CC physiological interactions of the polypeptide. Vectors comprising the
XX CC nucleic acids encoding the polypeptides and cells genetically engineered
XX CC to express them are also useful for producing the proteins. The proteins
XX CC are useful in genetic vaccination, testing and therapy, and can be used
XX CC as nutritional supplements. They may be used to increase stem cell
XX CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
XX CC and/or nerve tissue growth or regeneration; immune suppression and/or
XX CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
XX CC AAU29510-AAU33304 represent the amino acid sequences of novel human
XX CC secreted proteins of the invention
XX SQ Sequence 80 AA;
SQ Query Match 100.0%; Score 50; DB 4; Length 80;
Best Local Similarity 64.3%; Pred. No. 0.44;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YXTFSXLIXIFQXX 14

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2005, 16:08:55 ; Search time 38 Seconds
(without alignments)
35.448 Million cell updates/sec

Title: US-10-663-215-6

Perfect score: 50

Sequence: 1 YXTFSXLIXIFQXX 14

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	848	2 A33810	band 3 anion trans
2	50	100.0	911	1 B3HU	band 3 anion trans
3	50	100.0	929	2 A25314	band 3 protein - m
4	44	88.0	1234	2 A34311	band 3-related pro
5	44	88.0	1237	2 A56764	band 3-related pro
6	44	88.0	1237	2 A31789	band 3-related pro
7	43	86.0	865	2 A25104	band 3 protein, no
8	43	86.0	922	2 A30816	band 3 anion trans
9	43	86.0	1240	2 S21086	anion exchange pro
10	40	80.0	664	2 S02116	RNA helicase WSS11
11	40	80.0	844	2 F50159	anion transporter
12	39	78.0	289	2 F88939	protein C05E4.5 [i
13	38	76.0	474	2 E90312	hypothetical prote
14	38	76.0	656	1 B70107	hypothetical prote
15	38	76.0	912	2 S59861	band 3 anion trans
16	38	76.0	918	2 S24318	band 3 anion trans
17	38	76.0	2136	2 A05037	hypothetical prote
18	37	74.0	159	2 D71500	hypothetical prote
19	37	74.0	333	2 A19325	hypothetical prote
20	37	74.0	885	2 G71608	ATP-dept. acyl-CoA
21	37	74.0	1068	2 S01519	hypothetical prote
22	36	72.0	117	2 T08709	hypothetical prote
23	36	72.0	153	2 S68406	vesicular integral
24	36	72.0	155	2 AG1005	Type III leger pe
25	36	72.0	204	2 G70470	TolQ homolog - Aqu
26	36	72.0	217	2 F64744	probable transport
27	36	72.0	217	2 H90553	probable transport
28	36	72.0	217	2 H85504	probable transport
29	36	72.0	217	2 AH0131	ABC transporter pe

30	36	72.0	306	2 AD2794	conserved hypothet
31	36	72.0	306	2 C97573	hypothetical prote
32	36	72.0	325	2 T33549	hypothetical prote
33	36	72.0	353	2 S44162	hypothetical prote
34	36	72.0	353	2 T27377	hypothetical prote
35	36	72.0	354	2 B37386	hypothetical prote
36	36	72.0	354	2 S02220	hypothetical prote
37	36	72.0	366	2 D83912	hypothetical prote
38	36	72.0	401	2 G84792	hypothetical prote
39	36	72.0	409	2 T19326	hypothetical prote
40	36	72.0	410	2 E72397	hypothetical prote
41	36	72.0	435	2 H90578	conserved hypothet
42	36	72.0	476	2 T46067	hypothetical prote
43	36	72.0	494	2 A12438	UDP-N-acetyluramo
44	36	72.0	652	2 S09133	NADH2 dehydrogenas
45	36	72.0	657	2 S04724	NADH2 dehydrogenas

ALIGNMENTS

RESULT 1

A33810 band 3 anion transport protein - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004

C:Accession: A33810

R:Kudrycki, K.E.; Shull, G.E.

J. Biol. Chem. 264, 8185-8192, 1989

A:Title: Primary structure of the rat kidney band 3 anion exchange protein deduced from c

A:Reference number: A33810; MUID:89255254; PMID:2722777

A:Accession: A33810

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-848 <UD>

A:Cross-references: UNIPROT:P23562; GB:J04793; NID:G203092; PIDN:AAA40800.1; PID:G203093

C:Superfamily: band 3 anion transport protein

C:Keywords: alternative splicing; transmembrane protein

Query Match 100.0%; Score 50; DB 2; Length 848;
Best Local Similarity 64.3%; Pred. No. 0.93;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 YXTFSXLIXIFQXX 14

Db 472 YETFSKLKIFQDY 485

RESULT 2

B3HU

N:Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion exchange

C:Species: Homo sapiens (man)

C>Date: 03-Aug-1984 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004

C:Accession: A36218; S03074; I39408; I39409; A92237; A26507; A92430; A90323; A28079; S05;

R:Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F.

Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9093, 1989

A:Title: Cloning and characterization of band 3, the human erythrocyte anion-exchange pr

A:Reference number: A36218; MUID:90083213; PMID:2594752

A:Accession: A36218

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-911 <LUX>

A:Cross-references: UNIPROT:P02730; GB:M27819; NID:G178215; PIDN:AAA35514.1; PID:G178216

R:anner, M.J.A.; Martin, P.G.; High, S.

Biochem. J. 256, 703-712, 1988

A:Title: The complete amino acid sequence of the human erythrocyte membrane anion-transp

A:Reference number: S03074; MUID:89134172; PMID:3223947

A:Accession: S03074

A:Molecule type: mRNA

A:Residues: 1-55, 'E', 57-911 <TAN>

A:Cross-references: EMBL:X12609; NID:G28713; PIDN:CAA31128.1; PID:G28714

R:Shove, L.C.; Ballantine, M.; Huebner, K.

R/Kang, D.; Okubo, K.; Hamaeaki, N.; Kuroda, N.; Shiraki, H.
J. Biol. Chem. 267, 19211-19217, 1992
A;Title: A structural study of the membrane domain of band 3 by tryptic digestion. Confor
A;Reference number: A44116; MUID:92406862; PMID:1527044
A;Accession: A44116
A;Status: preliminary
A;Molecule type: protein
A;Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826 <KAN
A;Experimental source: erythrocyte
A;Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:113821, NCBIP:113823,
A;Note: a histidine residue essential for anion transport is suggested to be His-651, His
R/Okubo, K.; Kang, D.; Hamaeaki, N.; Jennings, M.L.
J. Biol. Chem. 269, 1918-1926, 1994
A;Title: Red blood cell band 3. Lysine 539 and lysine 851 react with the same H-2DIDS (4,
A;Reference number: A49717; MUID:94124538; PMID:8294441
A;Accession: A49717
A;Molecule type: protein
A;Residues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857 <OKU>
A;Note: Lys-539 and Lys-851 were shown to bind the same molecule of the anion transport
R/Hamaeaki, N.; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.
J. Biochem. 122, 577-585, 1997
A;Title: Proteolytic cleavage sites of band 3 protein in alkali-treated membranes: Fide
A;Reference number: PC4403; MUID:98006310; PMID:9348087
A;Accession: PC4403
A;Molecule type: protein
A;Residues: 361-911 <HAM>
C;Comment: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A dime
C;Comment: Band 3 has at least two functional domains. Its integral domain mediates a 1:1
ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.
C;Genetics:
A;Gene: GDB:SLC4A1; EPB3
A;Cross-references: GDB:119874; OMIM:109270
A;Map position: 17q21-17q22
C;Superfamily: band 3 anion transport protein
C;Keywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; transmembr
F/1-403/Region: cytoskeletal protein binding
F/404-911/Region: anion transporter
F/405-427/Domain: transmembrane #status predicted <TM01>
F/435-457/Domain: transmembrane #status predicted <TM02>
F/459-479/Domain: transmembrane #status predicted <TM03>
F/491-507/Domain: transmembrane #status predicted <TM04>
F/522-542/Domain: transmembrane #status predicted <TM05>
F/568-588/Domain: transmembrane #status predicted <TM06>
F/604-624/Domain: transmembrane #status predicted <TM07>
F/659-680/Domain: transmembrane #status predicted <TM08>
F/701-721/Domain: transmembrane #status predicted <TM09>
F/723-743/Domain: transmembrane #status predicted <TM10>
F/764-780/Domain: transmembrane #status predicted <TM11>
F/785-806/Domain: transmembrane #status predicted <TM12>
F/839-859/Domain: transmembrane #status predicted <TM13>
F/861-881/Domain: transmembrane #status predicted <TM14>
F/1/Modified site: acetylated amino end (Met) #status experimental
F/539,590,951/Binding site: anion (lys) #status experimental
F/642/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 50; DB 1; Length 911;
Best Local Similarity 64.3%; Pred. No. 0.99;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 YXTFSXLIXIFQXX 14
|:|:|:|:|:|:|:
DB 534 YETFSKLIXIFQDH 547

RESULT 3
A25314
band 3 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Jul-1997 #sequence revision 22-Jul-1997 #text_change 09-Jul-2004
C;Accession: A25314; A26086; I49524; B25104
R/Kopito, R.R.; Lodish, H.F.
Nature 316, 234-238, 1985
A;Title: Primary structure and transmembrane orientation of the murine anion exchange-pr

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OM protein - protein search, using sw model

Run on: August 26, 2005, 16:08:30 ; Search time 42 Seconds
(without alignments)
24.883 Million cell updates/sec

Title: US-10-663-215-6

Perfect score: 50

Sequence: 1 YXTFSLXLIIFQXX 14

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	58	3	US-08-405-647B-41
2	50	100.0	58	3	US-08-985-499-41
3	50	100.0	58	5	PCT-US96-03180-41
4	39	78.0	221	4	US-09-489-039A-12495
5	39	78.0	419	4	US-09-893-737-106
6	37	74.0	368	4	US-09-248-796A-20724
7	36	72.0	60	4	US-09-248-796A-26042
8	36	72.0	89	4	US-09-621-976-7593
9	36	72.0	341	4	US-09-489-039A-8294
10	36	72.0	354	3	US-08-969-644-10
11	36	72.0	354	3	US-08-444-189-10
12	36	72.0	354	3	US-08-468-544-10
13	36	72.0	384	4	US-09-491-577-16
14	36	72.0	540	4	US-09-248-796A-16674
15	36	72.0	1232	4	US-09-248-796A-14563
16	35	70.0	73	4	US-09-248-796A-27471
17	35	70.0	98	4	US-09-248-796A-23820
18	35	70.0	265	4	US-09-861-451A-74
19	35	70.0	298	4	US-09-270-767-34605
20	35	70.0	298	4	US-09-270-767-49822
21	35	70.0	350	4	US-09-107-433-3158
22	35	70.0	383	4	US-09-583-110-3277
23	35	70.0	426	4	US-09-489-039A-12211
24	35	70.0	545	4	US-09-270-767-58384
25	35	70.0	1088	4	US-09-270-767-43052
26	35	70.0	2357	4	US-09-949-016-9656
27	34	68.0	55	4	US-09-489-847-180

28	34	68.0	104	4	US-09-248-796A-23619	Sequence 23619, A
29	34	68.0	117	4	US-09-543-681A-6635	Sequence 6635, Ap
30	34	68.0	202	4	US-08-388-852B-38	Sequence 38, Appl
31	34	68.0	238	4	US-09-248-796A-19962	Sequence 19962, A
32	34	68.0	241	4	US-09-583-110-3990	Sequence 3990, Ap
33	34	68.0	243	4	US-09-107-433-4855	Sequence 4855, Ap
34	34	68.0	317	4	US-09-248-796A-15982	Sequence 15982, A
35	34	68.0	336	4	US-09-270-767-34164	Sequence 34164, A
36	34	68.0	336	4	US-09-270-767-49381	Sequence 49381, A
37	34	68.0	343	4	US-09-248-796A-19126	Sequence 19126, A
38	34	68.0	440	4	US-09-270-767-35908	Sequence 35908, A
39	34	68.0	440	4	US-09-270-767-51125	Sequence 51125, A
40	34	68.0	469	4	US-09-489-039A-9091	Sequence 9091, Ap
41	34	68.0	471	4	US-09-270-767-41444	Sequence 41444, A
42	34	68.0	495	4	US-09-991-552-20	Sequence 20, Appl
43	34	68.0	531	4	US-09-489-039A-12406	Sequence 12406, A
44	34	68.0	545	4	US-09-328-352-6221	Sequence 6221, Ap
45	34	68.0	611	4	US-09-248-796A-20762	Sequence 20762, A

ALIGNMENTS

RESULT 1
US-08-405-647B-41
; Sequence 41, Application US/08405647B
; Patent No. 6124262
; GENERAL INFORMATION:
; APPLICANT: Sherman, Irwin W.
; APPLICANT: Crandall, Ian E.
; APPLICANT: Sholet, Stephen B.
; APPLICANT: Thevenin, Bernard Jean-Marie
; TITLE OF INVENTION: Compositions and Methods for Reducing
; TITLE OF INVENTION: Adhesiveness of Defective Red Blood Cells
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,647B
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 02307E-068700US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-405-647B-41

Query Match 100.0%; Score 50; DB 3; Length 58;
Best Local Similarity 64.3%; Pred. No. 0.085;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 YXTFSLXLIIFQXX 14
|:||||:||||:|

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OM protein - protein search, using sw model

Run on: August 26, 2005, 16:09:55 ; Search time 160 Seconds
(without alignments)
34.381 Million cell updates/sec

Title: US-10-663-215-6

Perfect score: 50

Sequence: 1 YXTFSKLI1XIFQXX 14

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 1767149

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pdb.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pdb.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pdb.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pdb.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pdb.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pdb.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pdb.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pdb.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	14	17	US-10-663-215-5
2	50	100.0	14	17	US-10-663-215-6
3	50	100.0	911	14	US-10-066-320-2
4	50	100.0	911	14	US-10-087-464-6
5	50	100.0	911	14	US-10-087-464-8
6	50	100.0	911	16	US-10-408-765A-3
7	50	100.0	911	16	US-10-408-765A-500
8	50	100.0	911	16	US-10-643-795A-90
9	50	100.0	911	17	US-10-663-215-1
10	50	100.0	911	17	US-10-948-518-90
11	41	82.0	713	14	US-10-128-202-4
					Sequence 5, Appli
					Sequence 6, Appli
					Sequence 2, Appli
					Sequence 6, Appli
					Sequence 8, Appli
					Sequence 3, Appli
					Sequence 500, App
					Sequence 90, Appl
					Sequence 1, Appli
					Sequence 90, Appl
					Sequence 4, Appli

12	40	80.0	10	17	US-10-663-215-3	Sequence 3, Appli
13	40	80.0	10	17	US-10-663-215-4	Sequence 4, Appli
14	40	80.0	10	17	US-10-663-215-7	Sequence 7, Appli
15	40	80.0	10	17	US-10-663-215-8	Sequence 8, Appli
16	40	80.0	10	17	US-10-663-215-9	Sequence 9, Appli
17	40	80.0	10	17	US-10-663-215-10	Sequence 10, Appli
18	40	80.0	10	17	US-10-663-215-11	Sequence 11, Appli
19	40	80.0	10	17	US-10-663-215-12	Sequence 12, Appli
20	40	80.0	10	17	US-10-663-215-13	Sequence 13, Appli
21	40	80.0	10	17	US-10-663-215-14	Sequence 14, Appli
22	40	80.0	54	16	US-10-425-115-252138	Sequence 252138,
23	40	80.0	426	16	US-10-437-963-127713	Sequence 127713,
24	40	80.0	684	15	US-10-369-493-1654	Sequence 1654, Ap
25	40	80.0	664	18	US-10-972-963-166	Sequence 166, App
26	39	78.0	10	17	US-10-663-215-19	Sequence 19, Appl
27	39	78.0	39	16	US-10-437-963-190590	Sequence 190590,
28	39	78.0	55	16	US-10-437-963-200993	Sequence 200993,
29	39	78.0	217	15	US-10-282-122A-55827	Sequence 55827, A
30	39	78.0	217	15	US-10-282-122A-59599	Sequence 59599, A
31	39	78.0	419	9	US-09-893-737-106	Sequence 106, App
32	38	76.0	10	17	US-10-663-215-17	Sequence 17, Appl
33	38	76.0	37	15	US-10-424-599-177158	Sequence 177158,
34	38	76.0	52	15	US-10-424-599-213500	Sequence 213500,
35	38	76.0	54	15	US-10-424-599-282929	Sequence 282929,
36	38	76.0	64	15	US-10-424-599-181762	Sequence 181762,
37	38	76.0	79	16	US-10-425-115-360612	Sequence 360612,
38	38	76.0	132	15	US-10-424-599-145382	Sequence 145382,
39	38	76.0	188	16	US-10-425-115-313891	Sequence 313891,
40	38	76.0	438	16	US-10-425-115-297771	Sequence 297771,
41	38	76.0	475	16	US-10-425-115-297768	Sequence 297768,
42	38	76.0	486	15	US-10-425-114-39247	Sequence 39247, A
43	38	76.0	486	15	US-10-425-114-50309	Sequence 50309, A
44	38	76.0	487	15	US-10-425-114-68137	Sequence 68137, A
45	38	76.0	491	15	US-10-425-114-43004	Sequence 43004, A

ALIGNMENTS

RESULT 1

US-10-663-215-5
; Sequence 5, Application US/10663215
; Publication No. US20050059588A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Irwin
; APPLICANT: Winograd, Enrique
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Peptides Which Generate Antibodies Resulting in Lysis
; FILE REFERENCE: 023070-140500US
; CURRENT APPLICATION NUMBER: US/10/663,215
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: preferred
; OTHER INFORMATION: native AEL sequence, peptide including two
; OTHER INFORMATION: residues on either side of predicted alpha-helix
US-10-663-215-5

Query Match 100.0%; Score 50; DB 17; Length 14;
Best Local Similarity 64.3%; Pred. No. 0.25;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YXTFSKLI1XIFQXX 14

Db 1 YETFSKLI1KIFQDH 14

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OM protein - protein search, using sw model

Run on: August 26, 2005, 16:00:08 ; Search time 159 Seconds
(without alignments)
34.054 Million cell updates/sec

Title: US-10-663-215-6

Perfect score: 14

Sequence: 1 YXTPSLXIFQXX 14

Scoring table: OLIGODX

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 343861

Minimum DB seq length: 14

Maximum DB seq length: 40

Post-processing: Listing first 45 summaries

Database : A Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	71.4	17	2	AAW18597 Aged band
2	9	64.3	15	2	AAW01065 Anion tra
3	9	64.3	15	4	AAW74851 Band 3 pr
4	9	64.3	31	5	ABJ04861 Human pro
5	8	57.1	15	4	AAW97256 Human sph
6	8	57.1	16	2	AAW18601 Aged band
7	8	57.1	18	2	AAW71942 ALEM pro
8	8	57.1	20	4	AAW65375 Human bra
9	8	57.1	24	2	AAW71296 GPV tande
10	7	50.0	14	5	AAE25490 CAP1-19 t
11	7	50.0	14	5	ABG67766 Human ADP
12	7	50.0	16	2	AAW34145 Variant h
13	7	50.0	18	2	AAW12714 Human 5'
14	7	50.0	22	3	AAW63091 Human sec
15	7	50.0	23	6	ABO12200 Human zin
16	7	50.0	27	6	ABB82732 Cav chann
17	7	50.0	27	7	ADB67823 Human lun
18	7	50.0	30	6	AAO16565 CFTR prot
19	7	50.0	35	4	AAE01291 Human gen
20	7	50.0	35	4	AAW77413 Human col
21	7	50.0	35	5	ABG63767 Human alb
22	7	50.0	35	6	ABR63700 Human bre
23	7	50.0	35	8	ADL77032 Albumin f
24	7	50.0	36	6	ABP80600 N. gonorr
25	7	50.0	37	5	ABB81125 Human Fbx

26	7	50.0	37	6	ABU01204	Abu01204 S. pneumo
27	7	50.0	39	4	AAW96316	AAW96316 Human rep
28	6	42.9	14	2	AAW49466	AAW49466 Sodium ch
29	6	42.9	14	2	AAW42046	AAW42046 Cortistat
30	6	42.9	14	2	AAW23256	AAW23256 Apolipopr
31	6	42.9	14	2	AAW23259	AAW23259 Apolipopr
32	6	42.9	14	2	AAW23257	AAW23257 Apolipopr
33	6	42.9	14	2	AAW23254	AAW23254 Murine ap
34	6	42.9	14	2	AAW23258	AAW23258 Apolipopr
35	6	42.9	14	2	AAW73351	AAW73351 Monkey al
36	6	42.9	14	3	AAW07379	AAW07379 Monkey al
37	6	42.9	14	3	AAW26709	AAW26709 ATM kinas
38	6	42.9	14	4	AAW97055	AAW97055 Human pep
39	6	42.9	14	4	AAW98601	AAW98601 Human pep
40	6	42.9	14	4	AAW98010	AAW98010 Human SNP
41	6	42.9	14	5	AAW79480	AAW79480 Epitopic
42	6	42.9	14	5	ABG61488	ABG61488 Monkey Be
43	6	42.9	14	5	ABU51128	ABU51128 Helicobac
44	6	42.9	14	5	AAE21884	AAE21884 Cortistat
45	6	42.9	14	5	ABB05528	ABB05528 Biotinyla

ALIGNMENTS

RESULT 1
AAW18597
ID AAW18597 standard; peptide; 17 AA.
XX
AC AAW18597;
XX
DT 04-MAR-1998 (first entry)
XX
DE Aged band 3 peptide (residues 538-554) epitope IV.
XX
KW Band 3 protein; antibody; aging antigenic site; Alzheimer's disease;
KW phosphorylation; detection; epitope.
XX
OS Homo sapiens.
XX
PN WQ9726537-A1.
XX
PD 24-JUL-1997.
XX
PF 13-DEC-1996; 96WO-US020465.
XX
PR 19-JAN-1996; 96US-0010250P.
XX
PA (RESE) RESEARCH CORP TECHNOLOGIES INC.
XX
PI Kay MMB;
XX
DR WPI; 1997-395478/35.
XX
PT Detecting Alzheimer's disease using antibody that recognises aged band 3
PT protein in tissues - or from reduced degree of band 3 protein
PT phosphorylation, can be applied to blood or brain samples.
XX
PS Claim 10; Page 10; 45pp; English.
XX
CC This is an aging antigenic band 3 peptide (residues 538-554) to which a
CC specific antibody can bind to. Band 3 is a ubiquitous anion-exchange
CC protein and ages as cells and tissues age. Antibodies have been developed
CC against this aged band 3. These antibodies bind to distinct regions of
CC band 3 in old cells (aging antigenic sites) but not middle aged or young
CC cells. This can be used for detecting Alzheimer's disease. A tissue
CC sample containing band 3 from a patient suspected of having Alzheimer's
CC disease is treated with an antibody that can differentiate between the
CC Alzheimer's (aged) and normal band 3, under complex-forming conditions
CC and detecting any complex formed. A tissue containing band 3 from a
CC healthy control is treated in a similar manner and the amounts of complex
CC formed are compared. A significantly greater formation of complex in the
CC suspect sample as compared with that of the control is indicative of

CC Alzheimer's disease. The disease can also be detected by comparing the
 CC degrees of phosphorylation of band 3 or its degradation products in
 CC suspect and control samples. A significant decrease in phosphorylation in
 CC the suspect sample indicates Alzheimer's disease

XX SQ Sequence 17 AA;

Query Match 71.4%; Score 10; DB 2; Length 17;
 Best Local Similarity 60.0%; Pred. No. 0.3;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 5 SXLXIFQXX 14
 :||:||||:
 Db 1 SKLIKIFQDH 10

RESULT 2
 AAW01065
 ID AAW01065 standard; peptide; 15 AA.

XX AC AAW01065;

XX DT 08-MAY-1997 (first entry)

XX DE Anion transporter band 3 protein residues 539-553.

XX KW Anion transporter band 3 protein; endothelial adhesion; red blood cell;
 KW cytoplasmic domain; erythrocyte; exofacial loop; epitope; antibody;
 KW mammal; plasmodium falciparum infection; sickle cell disease; diabetes;
 KW band 3; thalassaemia; anaemia; therapy.

XX OS Synthetic.

XX PN WO9629086-A1.

XX PD 26-SEP-1996.

XX PF 07-MAR-1996; 96WO-US003180.

XX PR 17-MAR-1995; 95US-00405647.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Sherman IW, Crandall IE, Shohet SB, Thevenin BU;

XX DR WPI; 1996-442944/44.

XX PT Peptide(s) with amino acid motifs in band 3 - used for reducing the
 PT adhesiveness of red blood cells for treating malaria, sickle cell
 PT disease, thalassaemia or diabetes.

XX PS Claim 17; Page 39; 48pp; English.

XX CC AAW01053-W01095 represent peptides isolated from (or based on) regions of
 CC the anion transporter band 3 protein. The band 3 protein is present in a
 CC million copies per red blood cell, in the form of monomers, dimers, or
 CC tetramers. Band 3 protein has two distinct domains, a 43 kD water-soluble
 CC cytoplasmic domain, and a 55 kD membrane spanning domain. In an number of
 CC otherwise-unrelated conditions (such as malaria, and diabetes), there are
 CC modifications in band 3, such that there is clustering and a change in
 CC the conformation of the protein. Due to this change in protein
 CC conformation (and by the exposure of cryptic adhesive sites), the
 CC normally non-adherent erythrocyte becomes a cell with enhanced
 CC endothelial adhesiveness. These sequences were found in the putative
 CC exofacial loops of band 3, and are epitopes for antibody binding. These
 CC sequences compete with the altered band 3 protein, and thereby block the
 CC adhesiveness of the red blood cells. The peptides can be used for
 CC reducing the adhesiveness of red blood cells in a mammalian patient
 CC characterised by a condition selected from Plasmodium falciparum
 CC infection, sickle cell disease, thalassaemia and diabetes

XX SQ Sequence 15 AA;

Query Match 64.3%; Score 9; DB 2; Length 15;
 Best Local Similarity 55.6%; Pred. No. 2;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 6 XLXIFQXX 14
 :||:||||:
 Db 1 KLXIFQKH 9

RESULT 3
 AAB74851
 ID AAB74851 standard; peptide; 15 AA.

XX AC AAB74851;

XX DT 19-JUN-2001 (first entry)

XX DE Band 3 protein-ligand interaction inhibitor peptide SEQ ID NO:8.

XX KW Anti-Plasmodium falciparum; interaction inhibitor; band 3 protein;
 KW thrombolysis; thrombolytic; fibrinolytic; acute myocardial infarction;
 KW lysis; ventricular function; congestive heart failure; mortality;
 KW acute arterial thrombosis; embolism; thrombosis; cerebral sinus.

XX OS Synthetic.

XX PN US6191103-B1.

XX PD 20-FEB-2001.

XX PF 05-DEC-1997; 97US-00985499.

XX PR 05-DEC-1997; 97US-00985499.

XX PA (REGC) UNIV CALIFORNIA.

XX PI (BLOO-) CENT BLOOD RES.

XX PI Shohet SB, Sherman I, Von Andrian U;

XX DR WPI; 2001-307101/32.

XX PT Enhancing thrombolysis in mammals comprises administering an inhibitor of
 PT protein band 3-ligand interaction.

XX PS Claim 28; Col 42; 23pp; English.

XX CC The present invention describes a method for enhancing thrombolysis in a
 CC mammal. The method comprises the administration to the mammal an amount
 CC of an inhibitor (I) of protein band 3-ligand interaction sufficient to
 CC enhance thrombolysis. (I) has thrombolytic activity. The method is useful
 CC for enhancing thrombolysis in a mammal. (I) is useful for enhancing
 CC fibrinolytic or thrombolytic activity, in the management of acute
 CC myocardial infarction, for lysis of intracoronary thrombi, for
 CC improvement of ventricular function, for reduction of congestive heart
 CC failure, for reduction of mortality, for the lysis of pulmonary emboli
 CC blocking blood flow to one or more lobes of the lung, for the lysis of
 CC acute arterial thrombosis and embolism, for the lysis of thrombosis in
 CC deep veins or in cerebral sinuses, to reopen i.v. catheters obstructed by
 CC clotted blood or fibrin, to prevent clot formation of lysing clots, to
 CC prevent clotting in blood samples drawn from patients for clinical
 CC testing and to prevent the recurrence of thrombosis in patients by
 CC prophylactic administration. The present sequence represents a band 3
 CC protein-ligand interaction inhibitor peptide, which is used in the
 CC exemplification of the present invention

XX SQ Sequence 15 AA;

Query Match 64.3%; Score 9; DB 4; Length 15;
 Best Local Similarity 55.6%; Pred. No. 2;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 6 XLXIFQXX 14
 :||:||||:
 Db 1 KLXIFQKH 9

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OM protein - protein search, using sw model

Run on: August 26, 2005, 16:00:48 ; Search time 16 Seconds
(without alignments)
84.190 Million cell updates/sec

Title: US-10-663-215-6

Perfect score: 14

Sequence: 1 YXTFSXLIXIFQXX 14

Scoring table: OLIGODX

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 7379

Minimum DB seq length: 14

Maximum DB seq length: 40

Post-processing: Listing first 45 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	50.0	19	2 S01203	patatin (clone LPO
2	7	50.0	23	2 S00921	patatin (clone LPO
3	7	50.0	24	2 D83717	hypothetical prote
4	7	50.0	37	2 C95094	hypothetical prote
5	6	42.9	15	2 PA0110	translation elonga
6	6	42.9	20	2 H22565	R-phycoerythrin ga
7	6	42.9	23	2 S13298	benzaldehyde dehyd
8	6	42.9	27	2 S78355	hypothetical prote
9	6	42.9	29	2 T52557	translation elonga
10	6	42.9	29	2 A55891	delta-conotoxin Gm
11	6	42.9	30	2 S14214	NADH2 dehydrogenas
12	6	42.9	30	2 S07065	rRNA N-glycosidase
13	6	42.9	30	2 B70165	hypothetical prote
14	6	42.9	30	2 B81956	hypothetical prote
15	6	42.9	30	2 C71309	hypothetical prote
16	6	42.9	32	2 C56649	streptomycin 8-lik
17	6	42.9	32	2 B95081	hypothetical prote
18	6	42.9	33	2 G70254	hypothetical prote
19	6	42.9	33	2 D64543	hypothetical prote
20	6	42.9	33	2 C82312	hypothetical prote
21	6	42.9	34	2 G82502	hypothetical prote
22	6	42.9	35	2 AH1838	cytochrome c6 limp
23	6	42.9	37	2 S03674	photosystem I prot
24	6	42.9	38	2 D90631	hypothetical prote
25	6	42.9	38	2 G81904	hypothetical prote
26	6	42.9	38	2 A38335	58K tubulointersti
27	6	42.9	39	2 A81151	hypothetical prote
28	6	42.9	40	2 S05686	hypothetical prote
29	6	42.9	40	2 AH2446	hypothetical prote

30	5	35.7	14	2	G33160	H+-transporting tw
31	5	35.7	15	2	PH0782	T-cell receptor al
32	5	35.7	15	2	PN0629	integration host f
33	5	35.7	15	2	A60156	cellulase (BC 3.2.
34	5	35.7	15	2	PS0450	23K protein 4307 -
35	5	35.7	15	2	S62609	glutathione-disulf
36	5	35.7	16	2	B60566	cytochrome P450m51
37	5	35.7	16	2	S35627	uvrX protein - pha
38	5	35.7	16	2	S09700	phycobiliprotein 1
39	5	35.7	16	2	T09741	photosystem I chai
40	5	35.7	16	2	A26393	annexin 36K chain
41	5	35.7	16	2	PN0659	cytochrome P450 h-
42	5	35.7	16	2	A61268	cytochrome P450-th
43	5	35.7	18	1	DRUFPD	pigment-dispersing
44	5	35.7	18	2	A45590	beta-pigment-dipe
45	5	35.7	19	2	PC2326	proteasome endopep

ALIGNMENTS

RESULT 1

S01203

patatin (clone LPOt2) - potato (fragment)

C;Species: Solanum tuberosum (potato)

C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004

C;Accession: S01203

R;Twell, D.; Ooms, G.

Mol. Gen. Genet. 212, 325-336, 1988

A;Title: Structural diversity of the patatin gene family in potato cv. Desiree.

A;Reference number: S00921; MUID:88302122; PMID:2841572

A;Accession: S01203

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-19 <TWE>

A;Cross-references: UNIPROT:Q41466; EMBL:X07032; NID:g21506; PIDN:CAA30081.1; PID:g57948

C;Superfamily: patatin

Query Match 50.0%; Score 7; DB 2; Length 19;

Best Local Similarity 71.4%; Pred. No. 74;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SXLIXIF 11

Db 6 SFLILIF 12

RESULT 2

S00921

patatin (clone LPOt6) - potato (fragment)

C;Species: Solanum tuberosum (potato)

C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004

C;Accession: S00921

R;Twell, D.; Ooms, G.

Mol. Gen. Genet. 212, 325-336, 1988

A;Title: Structural diversity of the patatin gene family in potato cv. Desiree.

A;Reference number: S00921; MUID:88302122; PMID:2841572

A;Accession: S00921

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-23 <TWE>

A;Cross-references: UNIPROT:Q41464; EMBL:X07029

C;Genetics:

A;Start codon: GTG

C;Superfamily: patatin

Query Match 50.0%; Score 7; DB 2; Length 23;

Best Local Similarity 71.4%; Pred. No. 87;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SXLIXIF 11

Db 6 SFLILIF 12

RESULT 3
D83717
hypothetical protein BH0540 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: D83717
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: D83717
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-24 <STO>
A:Cross-references: UNIPROT:Q9KFE1; GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BA042
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0540

Query Match 50.0%; Score 7; DB 2; Length 24;
Best Local Similarity 71.4%; Pred. No. 90;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 5 SXLIXIF 11
Db 5 SLLIIF 11

RESULT 4
C95094
hypothetical protein SP0815 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: C95094
R:Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
neon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: C95094
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-37 <KUR>
A:Cross-references: UNIPROT:Q97RJ7; GB:AE005672; PIDN:AAK74948.1; PID:g14972289; GSPDB:C
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0815

Query Match 50.0%; Score 7; DB 2; Length 37;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 4 PSXLIXI 10
Db 23 PSYLIIGI 29

RESULT 5
PA0110
translation elongation factor eEF-1 beta' chain - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 07-Apr-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: PA0110
R:Kano, M.; Kawakami, T.; Tsugita, A.
submitted to JIPID, March 1995
A:Reference number: PA0109
A:Accession: PA0110
A:Molecule type: protein
A:Residues: 1-15 <KAM>

Query Match 42.9%; Score 6; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 2 XTFSXL 7
Db 2 VTFSDL 7

RESULT 6
H22565
R-phycoerythrin gamma-C chain - red alga (Gastrocionium coulteri) (fragment)
C:Species: Gastrocionium coulteri
C>Date: 07-Mar-1998 #sequence_revision 07-Mar-1998 #text_change 09-Jul-2004
C:Accession: H22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:95182601; PMID:3886644
A:Accession: H22565
A:Molecule type: protein
A:Residues: 1-20 <KLO>
A:Cross-references: UNIPROT:Q7M270
C:Superfamily: Aglaothamnion neglectum R-phycoerythrin gamma chain 33

Query Match 42.9%; Score 6; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 9 XIFQXX 14
Db 13 QIFQYP 18

RESULT 7
S13298
benzaldehyde dehydrogenase (EC 1.2.1.-) I - Acinetobacter calcoaceticus (fragment)
C:Species: Acinetobacter calcoaceticus
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 17-Mar-1999
C:Accession: S13298
R:Chalmers, R.M.; Keen, J.N.; Fewson, C.A.
Biochem. J. 273, 99-107, 1991
A:Title: Comparison of benzyl alcohol dehydrogenases and benzaldehyde dehydrogenases fro
uene pathway in Pseudomonas putida.
A:Reference number: S13298; MUID:91113163; PMID:1989592
A:Accession: S13298
A:Molecule type: protein
A:Residues: 1-23 <CHA>
A:Experimental source: NCIB 8250
C:Keywords: oxidoreductase

Query Match 42.9%; Score 6; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 9 XIFQXX 14
Db 15 HIFQGT 20

RESULT 8
S78355
hypothetical protein 27 - Odontella sinensis chloroplast
C:Species: chloroplast Odontella sinensis
C>Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 09-Jul-2004
C:Accession: S78355
R:Kowalik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
Plant Mol. Biol. Rep. 13, 336-342, 1995
A:Title: The Chloroplast Genome of a chlorophyll a+c- containing Alga, Odontella sinensis
A:Reference number: S78238
A:Accession: S78355

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OM protein - protein search, using sw model

Run on: August 26, 2005, 15:57:13 ; Search time 53 Seconds
(without alignments)
135.266 Million cell updates/sec

Title: US-10-663-215-6
Perfect score: 14
Sequence: 1 YTFSLXIXFOXX 14

Scoring table: OLIGODX
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 41659

Minimum DB seq length: 14
Maximum DB seq length: 40

Post-processing: Listing first 45 summaries

Database : Uniprot 03:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	57.1	20	Q9NZ27	Q9nz27 homo sapien
2	8	57.1	38	Q9B797	Q9b797 phalacrocor
3	7	50.0	19	Q41466	Q41466 solanum tub
4	7	50.0	19	Q41471	Q41471 solanum tub
5	7	50.0	20	Q41468	Q41468 solanum tub
6	7	50.0	20	Q41469	Q41469 solanum tub
7	7	50.0	23	Q41464	Q41464 solanum tub
8	7	50.0	24	Q9KPE1	Q9kpe1 bacillus ha
9	7	50.0	28	Q9UXE3	Q9uxr3 methanosaer
10	7	50.0	28	Q7RT34	Q7rt34 plasmodium
11	7	50.0	31	Q712K9	Q712k9 capra hircu
12	7	50.0	31	Q733P7	Q733p7 bacillus ce
13	7	50.0	33	Q9AY05	Q9ayg5 cucumis sat
14	7	50.0	36	Q83BA8	Q83ba8 cucuella bu
15	7	50.0	37	Q9ZR77	Q9zr77 streptococc
16	7	50.0	37	Q8F819	Q8f819 leptospira
17	7	50.0	38	Q8F466	Q8f466 leptospira
18	7	50.0	40	Q8NUM3	Q8num3 staphylococ
19	6	42.9	14	Q7S4U5	Q7s4u5 neorospira
20	6	42.9	15	Q9UCC4	Q9ucc4 homo sapien
21	6	42.9	16	P90290	P90290 barley mild
22	6	42.9	17	Q7Y834	Q7y834 cooperia on
23	6	42.9	17	Q7YAT7	Q7yat7 cooperia on
24	6	42.9	18	1 RIP_SIRGR	P83323 siraitia gr
25	6	42.9	18	Q71U72	Q71u72 homo sapien
26	6	42.9	19	Q41470	Q41470 solanum tub
27	6	42.9	20	Q9NZ28	Q9nz28 homo sapien
28	6	42.9	20	Q7RPN2	Q7rpn2 plasmodium
29	6	42.9	20	Q7M270	Q7m270 gastrocloni
30	6	42.9	20	Q9FPH8	Q9fph8 arabidopsis
31	6	42.9	20	P83065	P83065 bacillus ce

32	6	42.9	21	2	Q9FSA2	Q9fsa2 silene foet
33	6	42.9	21	2	O31349	O31349 bacillus ce
34	6	42.9	22	2	Q84172	Q84172 orf virus.
35	6	42.9	23	1	XYCI ACIGB	P46365 acinetobact
36	6	42.9	23	2	Q96TK6	Q96tk6 cryptococcu
37	6	42.9	24	2	Q817A6	Q817a6 penaeus van
38	6	42.9	24	2	Q817A7	Q817a7 litopenaeus
39	6	42.9	24	2	Q817A8	Q817a8 litopenaeus
40	6	42.9	24	2	Q817B1	Q817b1 farfantepen
41	6	42.9	24	2	Q7JPU0	Q7jpu0 drosophila
42	6	42.9	24	2	Q9BM17	Q9bm17 drosophila
43	6	42.9	24	2	O6JWP4	O6jwp4 trochodendr
44	6	42.9	25	2	O49748	O49748 arabidopsis
45	6	42.9	26	2	Q9BM15	Q9bm15 drosophila

ALIGNMENTS

RESULT 1
Q9NZ27 PRELIMINARY; PRT; 20 AA.
AC Q9NZ27;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE ATP7B (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu Z.Y., Wang N., MuRong S.X., Lin M.T., Fang L.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220213; AAF67659.1; -.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2365 MW; AAB07911D719FBF2 CRC64;

Query Match 57.1%; Score 8; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 91;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 XTFSLXIX 9
Db 3 HTFSVLIG 10
:|||||:

RESULT 2
Q9B797 PRELIMINARY; PRT; 38 AA.
AC Q9B797;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE ATPase 8 (Fragment).
OS Phalacrocorax purpurascens.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Pelecaniformes; Phalacrocoracidae;
OX NCBI_TaxID=146619;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20575768; PubMed=11133189; DOI=10.1006/mpev.2000.0840;
RA Kennedy M., Gray R.D., Spencer H.G.;
RT "The phylogenetic relationships of the shags and cormorants: can
sequence data resolve a disagreement between behavior and
morphology?";
RL Mol. Phylogenet. Evol. 17:345-359 (2000).
CC -!- FUNCTION: This is one of the chains of the nonenzymatic component
(CF(0) subunit) of the mitochondrial ATPase complex (By

```
CC similarity').
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -1- SUBCELLULAR LOCATION: Membrane-bound (By similarity).
CC EMBL: AY009358; AAG52926.1; -.
CC DR GO: GO:0005739; C:mitochondrion; IEA.
CC DR GO: GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
CC DR GO: GO:0046933; F:hydrogen-transporting ATP synthase activity; . . ; IEA.
CC DR GO: GO:0046961; F:hydrogen-transporting ATPase activity, rota. . . ; IEA.
CC DR GO: GO:0015986; P:ATP synthesis coupled proton transport; IEA.
CC DR GO: GO:0006811; P:ion transport; IEA.
CC DR GO: GO:0015992; P:proton transport; IEA.
CC DR InterPro: IPR001421; ATPase8 mit.
CC Pfam: PF00895; ATP-synt_8; 1_
KW CF(0); Hydrogen ion transport; Ion transport; Mitochondrion;
KW Transmembrane; transport.
FT NON_TER 1
SQ SEQUENCE 38 AA; 4433 MW; DB1B690DCC9B6C1 CRC64;

Query Match 57.1%; Score 8; DB 2; Length 38;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 XTFSKLIX 9
Db 1 LTFSLLIQ 8

RESULT 3
Q41466 ID Q41466 PRELIMINARY; PRT; 19 AA.
AC Q41466;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Potato class II patatin gene (LPOT2) (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=cultiv. Desiree.
RX MEDLINE=88302122; PubMed=2841572;
RA Twell D., Ooms G.;
RT "Structural diversity of the patatin gene family in potato cv.
RT Desiree.";
RL Mol. Gen. Genet. 212:325-336(1988).
DR EMBL: X07032; CAA30081.1; -.
DR PIR: S01203; S01203.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2135 MW; AF732E1FCDBE117E CRC64;

Query Match 50.0%; Score 7; DB 2; Length 19;
Best Local Similarity 71.4%; Pred. No. 5.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SXLIIXIF 11
Db 6 SFLILIF 12

RESULT 4
Q41471 ID Q41471 PRELIMINARY; PRT; 19 AA.
AC Q41471;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Potato patatin class II (Fragment).
OS Solanum tuberosum (Potato).

similarity').
-1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
H(+) (Out).
-1- SUBCELLULAR LOCATION: Membrane-bound (By similarity).
EMBL: AY009358; AAG52926.1; -.
DR GO: GO:0005739; C:mitochondrion; IEA.
DR GO: GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
DR GO: GO:0046933; F:hydrogen-transporting ATP synthase activity; . . ; IEA.
DR GO: GO:0046961; F:hydrogen-transporting ATPase activity, rota. . . ; IEA.
DR GO: GO:0015986; P:ATP synthesis coupled proton transport; IEA.
DR GO: GO:0006811; P:ion transport; IEA.
DR GO: GO:0015992; P:proton transport; IEA.
DR InterPro: IPR001421; ATPase8 mit.
DR Pfam: PF00895; ATP-synt_8; 1_
KW CF(0); Hydrogen ion transport; Ion transport; Mitochondrion;
KW Transmembrane; transport.
FT NON_TER 1
SQ SEQUENCE 38 AA; 4433 MW; DB1B690DCC9B6C1 CRC64;

Query Match 57.1%; Score 8; DB 2; Length 38;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 XTFSKLIX 9
Db 1 LTFSLLIQ 8

RESULT 3
Q41466 ID Q41466 PRELIMINARY; PRT; 19 AA.
AC Q41466;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Potato class II patatin gene (LPOT2) (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=cultiv. Desiree.
RX MEDLINE=88302122; PubMed=2841572;
RA Twell D., Ooms G.;
RT "Structural diversity of the patatin gene family in potato cv.
RT Desiree.";
RL Mol. Gen. Genet. 212:325-336(1988).
DR EMBL: X07032; CAA30081.1; -.
DR PIR: S01203; S01203.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2135 MW; AF732E1FCDBE117E CRC64;

Query Match 50.0%; Score 7; DB 2; Length 19;
Best Local Similarity 71.4%; Pred. No. 5.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SXLIIXIF 11
Db 6 SFLILIF 12

RESULT 4
Q41471 ID Q41471 PRELIMINARY; PRT; 19 AA.
AC Q41471;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Potato patatin class II (Fragment).
OS Solanum tuberosum (Potato).
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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=88226014; PubMed=3371664; DOI=10.1016/0378-1119(88)90577-X;
RA Mignery G.A., Pikaard C.S., Park W.D.;
RT "Molecular characterization of the patatin multigene family of
RT potato.";
RL Gene 62:27-44(1988).
DR EMBL: M18885; AAA33833.1; -.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2103 MW; AB632E1FCDB8D17E CRC64;

Query Match 50.0%; Score 7; DB 2; Length 19;
Best Local Similarity 71.4%; Pred. No. 5.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SXLIIXIF 11
Db 6 SFLILIF 12

RESULT 5
Q41468 ID Q41468 PRELIMINARY; PRT; 20 AA.
AC Q41468;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Potato patatin (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=88302122; PubMed=2841572;
RA Twell D., Ooms G.;
RT "Structural diversity of the patatin gene family in potato cv.
RT Desiree.";
RL Mol. Gen. Genet. 212:325-336(1988).
DR EMBL: M37223; AAA33821.1; -.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2222 MW; 3C5F732E1FCDBE11 CRC64;

Query Match 50.0%; Score 7; DB 2; Length 20;
Best Local Similarity 71.4%; Pred. No. 5.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SXLIIXIF 11
Db 6 SFLILIF 12

RESULT 6
Q41469 ID Q41469 PRELIMINARY; PRT; 20 AA.
AC Q41469;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Patatin (fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Desiree;
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OM protein - protein search, using sw model

Run on: August 26, 2005, 16:01:39 ; Search time 21 Seconds
(without alignments)
49.766 Million cell updates/sec

Title: US-10-663-215-6

Perfect score: 14

Sequence: 1 YXFSXLIXFOXX 14

Scoring table: OLIGODX

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 118471

Minimum DB seq length: 14

Maximum DB seq length: 40

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	64.3	15	3	US-08-405-647B-8
2	9	64.3	15	3	US-08-985-499-8
3	9	64.3	15	5	PCT-US96-03180-8
4	8	57.1	24	3	US-08-592-500-23
5	8	57.1	24	3	US-08-195-006-23
6	8	57.1	24	5	PCT-US94-07644A-23
7	7	50.0	16	3	US-08-336-643A-79
8	7	50.0	23	4	US-08-270-767-62060
9	7	50.0	25	4	US-08-987-685A-42
10	7	50.0	25	4	US-08-086-436-49
11	7	50.0	25	4	US-08-270-767-46476
12	7	50.0	33	4	US-08-270-767-59072
13	7	50.0	40	4	US-08-270-767-35098
14	7	50.0	40	4	US-08-270-767-40885
15	7	50.0	40	4	US-08-270-767-50315
16	7	50.0	40	4	US-08-270-767-56101
17	6	42.9	14	2	US-08-480-190-176
18	6	42.9	14	2	US-08-943-363-109
19	6	42.9	14	2	US-08-488-379-176
20	6	42.9	14	3	US-08-648-322-24
21	6	42.9	14	3	US-08-193-043-109
22	6	42.9	14	3	US-08-400-653A-7
23	6	42.9	14	3	US-08-248-061B-7
24	6	42.9	14	4	US-08-688-307A-109
25	6	42.9	14	4	US-08-857-389-24
26	6	42.9	14	4	US-08-475-399A-176
27	6	42.9	14	4	US-08-350-259-109

Sequence 1, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 12, Appli
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Sequence 14, Appli
Sequence 18, Appli
Sequence 19, Appli
Sequence 20, Appli
Sequence 176, App
Sequence 26, Appli
Sequence 24, Appli
Sequence 176, App
Sequence 1, Appli
Sequence 4, Appli
Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-405-647B-8
; Sequence 8, Application US/08405647B
; Patent No. 6124262
; GENERAL INFORMATION:
; APPLICANT: Sherman, Irwin W.
; APPLICANT: Crandall, Ian E.
; APPLICANT: Sholet, Stephen B.
; APPLICANT: Thevenin, Bernard Jean-Marie
; TITLE OF INVENTION: Compositions and Methods for Reducing
; TITLE OF INVENTION: Adhesiveness of Defective Red Blood Cells
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,647B
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 02307E-068700US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-405-647B-8

Query Match 64.3%; Score 9; DB 3; Length 15;
Best Local Similarity 55.6%; Pred. No. 0.47;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 XLIXIFOXX 14
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Db      1 KLIKIFQKH 9

RESULT 2
US-08-985-499-8
; Sequence 8, Application US/08985499
; Patent No. 6191103
; GENERAL INFORMATION:
; APPLICANT: Shohet, Stephen B.
; APPLICANT: Sherman, Irwin
; APPLICANT: von Andrian, Ulrich
; TITLE OF INVENTION: Methods for Enhancing Thrombolysis in a
; TITLE OF INVENTION: Mammal
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,499
; FILING DATE: 05-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hyman, Laurence J.
; REGISTRATION NUMBER: 35,551
; REFERENCE/DOCKET NUMBER: 02307E-084500US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US96-03180-8
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/03180
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-370
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US96-03180-8
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/03180
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 12418-28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide

Query Match 64.3%; Score 9; DB 5; Length 15;
Best Local Similarity 55.6%; Pred. No. 0.47;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      6 XLIXIFQXX 14
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Db      1 KLIKIFQKH 9

RESULT 4
US-08-592-500-23
; Sequence 23, Application US/08592500
; Patent No. 6005089
; GENERAL INFORMATION:
; APPLICANT: Lanza, Francois
; APPLICANT: Phillips, David R.
; APPLICANT: Casenave, Jean-Pierre
; TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,500
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,455
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 12418-28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide

Query Match 64.3%; Score 9; DB 3; Length 15;
Best Local Similarity 55.6%; Pred. No. 0.47;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      6 XLIXIFQXX 14
       :|:|:|:|:
Db      1 KLIKIFQKH 9

RESULT 3
PCT-US96-03180-8
; Sequence 8, Application PC/TUS9603180
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University
; APPLICANT: of California
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REDUCING
; TITLE OF INVENTION: ADHESIVENESS OF DEFECTIVE RED BLOOD CELLS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 North Figueroa Street, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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Result No.	Score	Query Match	Length	DB	ID	Description
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2	14	100.0	14	17	US-10-663-215-6	Sequence 6, Appli
3	9	64.3	31	13	US-10-001-879-140	Sequence 140, App
4	9	64.3	37	15	US-10-424-599-177158	Sequence 177158, A
5	8	57.1	20	9	US-09-864-761-46255	Sequence 46255, A
6	8	57.1	22	16	US-10-437-963-155966	Sequence 155966, A
7	8	57.1	24	14	US-10-212-499-23	Sequence 23, Appl
8	8	57.1	35	16	US-10-425-115-303352	Sequence 303352, A
9	7	50.0	14	14	US-10-014-340-520	Sequence 520, App
10	7	50.0	14	15	US-10-449-829A-30	Sequence 30, Appl
11	7	50.0	16	14	US-10-121-746-79	Sequence 79, Appl

Db 1 YETFSKLIKIFQDH 14

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RESULT 2
US-10-663-215-6
; Sequence 6, Application US/10663215
; Publication No. US20050059588A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Irwin
; APPLICANT: Winograd, Enrique
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Peptides Which Generate Antibodies Resulting in Lysis
; TITLE OF INVENTION: of Pathologically Adherent Erythrocytes
; FILE REFERENCE: 023070-140500US
; CURRENT APPLICATION NUMBER: US/10/663,215
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide mimic
; OTHER INFORMATION: when used as antigen raises antibodies which bind
; OTHER INFORMATION: to and cause destruction of pathologically
; OTHER INFORMATION: adherent erythrocytes
; NAME/KEY: MOD RES
; LOCATION: (1)..(14)
; OTHER INFORMATION: Xaa = amino acid charged under physiological
; OTHER INFORMATION: conditions
US-10-663-215-6

Query Match          100.0%; Score 14; DB 17; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YXTFSLXIFQXX 14
| | | | | | | | | |
Db 1 YXTFSLXIFQXX 14

RESULT 3
US-10-001-879-140
; Sequence 140, Application US/10001879
; Publication No. US20020127237A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Hervé
; APPLICANT: Cafferkey, Robert
; APPLICANT: Ali, Shujath
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
; FILE REFERENCE: DEX-0281
; CURRENT APPLICATION NUMBER: US/10/001,879
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,188
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 201
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 140
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-879-140

Query Match          64.3%; Score 9; DB 13; Length 31;
Best Local Similarity 55.6%; Pred. No. 11;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 XLXIFQXX 14
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Db 5 ILIFQNF 13
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RESULT 4
US-10-424-599-177158
; Sequence 177158, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 177158
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_130991C.1.pep
US-10-424-599-177158

Query Match          64.3%; Score 9; DB 15; Length 37;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YXTFSLXIX 9
| | | | | | | |
Db 21 YPTFSLXIY 29

RESULT 5
US-09-864-761-46255
; Sequence 46255, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
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